

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
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Harley, Calvin  
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(ii) TITLE OF INVENTION: Novel Telomerase

(iii) NUMBER OF SEQUENCES: 225

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: California  
(E) COUNTRY: United States of America  
(F) ZIP: 94111

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/854,050  
(B) FILING DATE: 09-MAY-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/851,843  
(B) FILING DATE: 06-MAY-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/846,017  
(B) FILING DATE: 25-APR-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/844,419  
(B) FILING DATE: 18-APR-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/724,643  
(B) FILING DATE: 01-OCT-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Apple, Randolph T.  
(B) REGISTRATION NUMBER: 36,429  
(C) REFERENCE/DOCKET NUMBER: 015389-002930US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAACCCCAA AACCCCAAAA CCCCTTTT TAG AGCCCTGCAG TTGGAAATAT AACCTCAGTA	60
TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA	120
TCAAGCTGAT AATCATGGCA TTCACTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC	180
TAAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA	240
TTATAAAGAT TTAGAAGATA TTAAATATT TGC GCAGACA AATATTGTTG C TACTCCACG	300
AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT	360
AATGATCGAA CTTATTGACA AATGCTTAGT TGA ACTTCTT TCATCAAGCG ATGTTTCAGA	420
TAGACAAAAA CTTCAATGAT TTGGATTTC AACTTAAGGGA AATCAATTAG CAAAGACCCA	480
TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT	540
TAGAGCAATG ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA	600
GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA	660
AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG	720
ATGTTGATCA ACCTGCAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT	780
CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT	840
TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTG TGAGTAACAAA ACAATATTTT	900
AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA	960
GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT	1020
TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGGAACGGAA	1080
ACAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA	1140
GCTGTTTAGC TACACAAC TGATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA	1200
CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT	1260
TAAGAAATAT GTGGAATAA ACAAGCATGA ACTCATTCAC AAAAATTAT TGCTTGAGAA	1320
GATCAATACA AGAGAAATAT CATGGATGCA GGTGAGACC TCTGCAAAGC ATTTTTATTA	1380
TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT	1440

CGTCGTCTCG	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA	1500
AACCTATTAC	TACAGAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA	TCGCAGACTT	1560
AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT	GAAGAATGGA	AAAAGTCGCT	1620
TGGATTTGCA	CCTGGAAAAC	TCAGACTAAT	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	1680
GACTTTCAAT	AAGAAGATTG	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	1740
GAAGTTATTG	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC	1800
TTTTGGATTG	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG	AGTTTGTTTG	1860
CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA	ACTATGGATA	TCGAAAAGTG	1920
ATATGATAGT	GTAAACAGAG	AAAAACTATC	AACATTCCCTA	AAAACTACTA	AATTACTTTC	1980
TTCAGATTTT	TGGATTATGA	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	2040
TTTCGAAAAAC	TTTAGAAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT	2100
TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAATG	AACAAAATGA	2160
CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA	AGAAATTATT	TTAAGAAAGA	2220
TAACCTACTT	CAACCAGTCA	TTAATATTTG	CCAATATAAT	TACATTAACT	TTAATGGGAA	2280
GTTTTATAAA	CAAACAAAAG	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTCATC	2340
ATTTTATTAT	GCAACATTAG	AGGAAAGCTC	CTTAGGATTG	CTTAGAGATG	AATCAATGAA	2400
CCCTGAAAAT	CCAAATGTGA	ATCTTCTAAT	GAGACTTACA	GATGACTATC	TTTTGATTAC	2460
AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAACTT	ATAAACGTAA	GTCGTGAAAA	2520
TGGATTTTAA	TTCAATATGA	AGAAACTACA	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	2580
TGCAAAATAC	GGAATGGATA	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	2640
GATTGGCATC	TCAATTGATA	TGAAAACCTC	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT	2700
AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT	CAATGTGGCT	2760
CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC	CATTATTTTA	GAAAGACGAT	2820
TACAACCGAA	GACTTTGCGA	ATAAACTCT	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	2880
ATACATGCAA	TGAGCCAAAG	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	2940
TATGATCGAC	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA	3000
CCTTGTTGTC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG	ACTTTTTCTT	3060
TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA	AAGTACATTT	TCAACAGAGT	3120
TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	3180
TCAATATGAT	GCATAGTCGA	CTATTCTAAC	TTATTTTGGA	AAGTTAATTT	TCAATTTTTG	3240
TCTTATATAC	TGGGGTTTTG	GGGTTTTGGG	GTTTTGGGG			3279

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Val	Asp	Val	Asp	Asn	Gln	Ala	Asp	Asn	His	Gly	Ile	His	Ser	1	5	10	15
Ala	Leu	Lys	Thr	Cys	Glu	Glu	Ile	Lys	Glu	Ala	Lys	Thr	Leu	Tyr	Ser	20	25	30	
Trp	Ile	Gln	Lys	Val	Ile	Arg	Cys	Arg	Asn	Gln	Ser	Gln	Ser	His	Tyr	35	40	45	
Lys	Asp	Leu	Glu	Asp	Ile	Lys	Ile	Phe	Ala	Gln	Thr	Asn	Ile	Val	Ala	50	55	60	
Thr	Pro	Arg	Asp	Tyr	Asn	Glu	Glu	Asp	Phe	Lys	Val	Ile	Ala	Arg	Lys	65	70	75	80
Glu	Val	Phe	Ser	Thr	Gly	Leu	Met	Ile	Glu	Leu	Ile	Asp	Lys	Cys	Leu	85	90	95	
Val	Glu	Leu	Leu	Ser	Ser	Ser	Asp	Val	Ser	Asp	Arg	Gln	Lys	Leu	Gln	100	105	110	
Cys	Phe	Gly	Phe	Gln	Leu	Lys	Gly	Asn	Gln	Leu	Ala	Lys	Thr	His	Leu	115	120	125	
Leu	Thr	Ala	Leu	Ser	Thr	Gln	Lys	Gln	Tyr	Phe	Phe	Gln	Asp	Glu	Trp	130	135	140	
Asn	Gln	Val	Arg	Ala	Met	Ile	Gly	Asn	Glu	Leu	Phe	Arg	His	Leu	Tyr	145	150	155	160
Thr	Lys	Tyr	Leu	Ile	Phe	Gln	Arg	Thr	Ser	Glu	Gly	Thr	Leu	Val	Gln	165	170	175	
Phe	Cys	Gly	Asn	Asn	Val	Phe	Asp	His	Leu	Lys	Val	Asn	Asp	Lys	Phe	180	185	190	
Asp	Lys	Lys	Gln	Lys	Gly	Gly	Ala	Ala	Asp	Met	Asn	Glu	Pro	Arg	Cys	195	200	205	
Cys	Ser	Thr	Cys	Lys	Tyr	Asn	Val	Lys	Asn	Glu	Lys	Asp	His	Phe	Leu	210	215	220	
Asn	Asn	Ile	Asn	Val	Pro	Asn	Trp	Asn	Asn	Met	Lys	Ser	Arg	Thr	Arg	225	230	235	240
Ile	Phe	Tyr	Cys	Thr	His	Phe	Asn	Arg	Asn	Asn	Gln	Phe	Phe	Lys	Lys	245	250	255	
His	Glu	Phe	Val	Ser	Asn	Lys	Asn	Asn	Ile	Ser	Ala	Met	Asp	Arg	Ala	260	265	270	



Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys  
275 280 285

Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val  
290 295 300

Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro  
305 310 315 320

Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys  
325 330 335

Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr  
340 345 350

Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn  
355 360 365

Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln  
370 375 380

Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His  
385 390 395 400

Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met  
405 410 415

Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn  
420 425 430

Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val  
435 440 445

Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser  
450 455 460

Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met  
465 470 475 480

Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln  
485 490 495

Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly  
500 505 510

Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr  
515 520 525

Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr  
530 535 540

Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys  
545 550 555 560

Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp  
565 570 575

Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val  
580 585 590

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr  
595 600 605

Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys  
 610 615 620  
 Leu Leu Ser Ser Asp Phe Trp Ile Met Thr Ala Gln Ile Leu Lys Arg  
 625 630 635 640  
 Lys Asn Asn Ile Val Ile Asp Ser Lys Asn Phe Arg Lys Lys Glu Met  
 645 650 655  
 Lys Asp Tyr Phe Arg Gln Lys Phe Gln Lys Ile Ala Leu Glu Gly Gly  
 660 665 670  
 Gln Tyr Pro Thr Leu Phe Ser Val Leu Glu Asn Glu Gln Asn Asp Leu  
 675 680 685  
 Asn Ala Lys Lys Thr Leu Ile Val Glu Ala Lys Gln Arg Asn Tyr Phe  
 690 695 700  
 Lys Lys Asp Asn Leu Leu Gln Pro Val Ile Asn Ile Cys Gln Tyr Asn  
 705 710 715 720  
 Tyr Ile Asn Phe Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro  
 725 730 735  
 Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr  
 740 745 750  
 Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro  
 755 760 765  
 Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu  
 770 775 780  
 Leu Ile Thr Thr Gln Glu Asn Asn Ala Val Leu Phe Ile Glu Lys Leu  
 785 790 795 800  
 Ile Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
 805 810 815  
 Gln Thr Ser Phe Pro Leu Ser Pro Ser Lys Phe Ala Lys Tyr Gly Met  
 820 825 830  
 Asp Ser Val Glu Glu Gln Asn Ile Val Gln Asp Tyr Cys Asp Trp Ile  
 835 840 845  
 Gly Ile Ser Ile Asp Met Lys Thr Leu Ala Leu Met Pro Asn Ile Asn  
 850 855 860  
 Leu Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr  
 865 870 875 880  
 Lys Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met  
 885 890 895  
 Asn Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe  
 900 905 910  
 Ala Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr  
 915 920 925  
 Met Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala  
 930 935 940

Met Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val  
 945 950 955 960

Thr Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile  
 965 970 975

Phe Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His  
 980 985 990

Phe Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys  
 995 1000 1005

Met Ile Leu Lys Ala Lys Glu Ala Lys Leu Lys Ser Asp Gln Cys Gln  
 1010 1015 1020

Ser Leu Ile Gln Tyr Asp Ala  
 1025 1030

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG GTAGTTTAGA	60
AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA TTTGGATGAT ATAGAAAATT	120
TACTTCCTAA TACATTCAAC AAGTATAGCA GCTCTTGTAG TGACAAGAAA GGATGCAAAA	180
CATTGAAATC TGGCTCGAAA TCGCCTTCAT TGA CTATTCC AAAGTTGCAA AAACAATTAG	240
AGTTCTACTT CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA	300
AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA AATCAGGTAA	360
TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA TTATGGAGAA AATTACTTAA	420
TACTAAAAGG TAAACAGTTT GGATTATTTT CCTAGCCAAC AATGATGAGT ATATTAAATT	480
CATATGAGAA TGAGTCAAAG GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT	540
AAAACGCAAG AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTA CTATTTCG	600
TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC TTGAGACAAT	660
TGAAAAAGCT GTTACAACCT GAAGGAATCG CAGTTCTGAA AGTTCTGATG TGTATGCCAT	720
TATTTTGTGA ATTAATCTCA AATATCTTAT CTCAATTTAA TGGATAGCTA TAGAAACAAA	780
CCAAATAAAC CATGCAAGTT TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC	840
TGAATTTATA TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC	900
TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT AAAAGAAGCA	960

GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT TTGTTGATTC TTCTGTAACC 1020  
GGAATTAACA ACAAGAATAT TAGCAACGAA AAAGAAGAAG AGCTATCACA ATCCTGATTC 1080  
TTAAAGATTT CAAAAATTCC AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG 1140  
TTTTTCATTT CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTTGA TTAGCTGGAA 1200  
GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT TCACATTCAT 1260  
AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA GCAGTCATCC GTTTTAAAAA 1320  
TAGTGCTATG AGGACTAAAT TTTTAGAGTC AAGAAATGGA GCCGAAATCT TAATCAAAAA 1380  
GAATTGCGTC GATATTGCAA AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA 1440  
ATCTTGATTG ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA 1500  
GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG CGATCTTCAA 1560  
TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA ATACAAACCT TGGTCAAAAT 1620  
ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA AAAGAAAAAA TAAGGCAATA AATAAAATGA 1680  
GTACAGAAGT GAAGAAATAA AAGATTTATT TTTTTCATAA ATTTATTGAA AAGAGGGGTT 1740  
TTGGGGTTTT GGGGTTTTTG GG 1762

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Pro Gln Asn Pro Lys Thr Pro Lys Pro Leu Lys Lys Lys Lys Leu Arg  
1 5 10 15  
Phe Arg Asn Lys Ile Leu Phe Pro His Lys Trp Arg Trp Ile Leu Ile  
20 25 30  
Trp Met Ile Lys Ile Tyr Phe Leu Ile His Ser Thr Ser Ile Ala Ala  
35 40 45  
Leu Val Val Thr Arg Lys Asp Ala Lys His Cys Asn Leu Ala Arg Asn  
50 55 60  
Arg Leu His Cys Leu Phe Gln Ser Cys Lys Asn Asn Ser Ser Thr Ser  
65 70 75 80  
Arg Met Gln Ile Phe Ile Thr Ile Leu Ser Cys Glu Asn Phe Lys Ala  
85 90 95  
Glu Ser Lys Glu Lys Leu Lys His Tyr Cys Leu Asn Lys Ile Arg Cys  
100 105 110  
Gly Leu Phe Tyr Phe Leu Asp His Phe Leu Arg Ser Ile Met Glu Lys

115					120					125					
Ile	Thr	Tyr	Lys	Val	Asn	Ser	Leu	Asp	Tyr	Phe	Pro	Ser	Gln	Gln	Cys
130						135					140				
Cys	Val	Tyr	Ile	His	Met	Arg	Met	Ser	Gln	Arg	Ile	Ser	Ile	His	Gln
145					150					155					160
Thr	Tyr	Gln	Arg	Gln	Thr	Arg	Tyr	Lys	Thr	Gln	Glu	Lys	Val	Cys	Ser
				165					170					175	
Asn	Ser	Arg	Arg	Thr	Tyr	Cys	Ile	Tyr	Tyr	Ser	Tyr	Gly	Phe	Tyr	Tyr
			180					185					190		
Asn	Cys	Phe	Arg	Tyr	Arg	Arg	Cys	Thr	Pro	Glu	Ser	Cys	Asp	Asn	Cys
		195					200					205			
Lys	Ser	Cys	Leu	Gln	Leu	Lys	Glu	Ser	Gln	Phe	Cys	Lys	Phe	Cys	Val
	210					215					220				
Cys	His	Tyr	Phe	Val	Asn	Ser	Gln	Ile	Ser	Tyr	Leu	Asn	Leu	Met	Asp
225					230					235					240
Ser	Tyr	Arg	Asn	Lys	Pro	Asn	Lys	Pro	Cys	Lys	Phe	Asn	Gly	Ile	Tyr
				245					250					255	
Val	Lys	Ser	Phe	Gly	Thr	Asn	Ala	His	Cys	Ile	Tyr	Ile	Gly	Phe	Leu
			260					265					270		
Lys	His	Arg	Tyr	Thr	Glu	Cys	Phe	Arg	Asp	Cys	Phe	Ser	Leu	Gln	Gln
		275					280					285			
Ile	Thr	Cys	Phe	Asp	Tyr	Ser	Cys	Ser	Ser	Leu	Ile	Ser	Leu	Lys	Glu
	290					295					300				
Ala	Gly	Glu	Met	Lys	Arg	Arg	Leu	Lys	Lys	Glu	Ile	Ser	Lys	Phe	Val
305					310					315					320
Asp	Ser	Ser	Val	Thr	Gly	Ile	Asn	Asn	Lys	Asn	Ile	Ser	Asn	Glu	Lys
				325					330					335	
Glu	Glu	Glu	Leu	Ser	Gln	Ser	Cys	Phe	Leu	Lys	Ile	Ser	Lys	Ile	Pro
			340					345					350		
Gly	Lys	Arg	Asp	Thr	Phe	Ile	Lys	Ile	His	Ile	Leu	Phe	Phe	Ile	Ser
		355					360					365			
Gln	Leu	Leu	Phe	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Phe	Asp	Leu	Glu	Val
	370					375					380				
Lys	Ser	Ile	Lys	Glu	Lys	Arg	Thr	Glu	Val	Thr	Leu	Ile	His	Ile	His
	385					390					395				400
Arg	Ser	Thr	Phe	Ile	Tyr	Pro	Ile	Arg	Cys	Gly	Asn	Ser	Ser	His	Pro
			405						410					415	
Phe	Lys	Cys	Tyr	Glu	Asp	Ile	Phe	Arg	Val	Lys	Lys	Trp	Ser	Arg	Asn
			420					425					430		
Leu	Asn	Gln	Lys	Glu	Leu	Arg	Arg	Tyr	Cys	Lys	Arg	Ile	Glu	Leu	Ile
	435						440					445			

Phe Arg Val Leu Pro Ile Leu Ile Asp Cys Arg Asp Arg Gly Asn Cys  
 450 455 460  
 Thr Glu Asp His Arg Asn Lys Val Thr Phe Ile Asn Arg Ile Asn Ile  
 465 470 475 480  
 Thr Asn Ile Glu Ile Ser Asp Leu Gln Leu Thr Lys Lys Leu Asn Ser  
 485 490 495  
 Thr Ile Lys Asn Thr Asn Leu Gly Gln Asn Ile Glu Glu Gly Lys Glu  
 500 505 510  
 Asp Gln Leu Ala Lys Glu Lys Ile Arg Gln Ile Lys Cys Val Gln Lys  
 515 520 525  
 Cys Arg Asn Lys Arg Phe Ile Phe Phe Asn Asn Leu Leu Lys Arg Gly  
 530 535 540  
 Val Leu Gly Phe Trp Gly Phe Gly  
 545 550

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 562 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Pro Lys Thr Pro Lys Pro Gln Asn Pro Tyr Lys Lys Arg Lys Asn Cys  
 1 5 10 15  
 Gly Ser Leu Glu Ile Lys Tyr Tyr Ser Arg Thr Asn Gly Asp Gly Tyr  
 20 25 30  
 Cys Phe Gly Cys Tyr Arg Lys Phe Thr Ser Tyr Ile Gln Gln Val Gln  
 35 40 45  
 Leu Leu Gln Glu Arg Met Gln Asn Ile Glu Ile Trp Leu Glu Ile Ala  
 50 55 60  
 Phe Ile Asp Tyr Ser Lys Val Ala Lys Thr Ile Arg Val Leu Leu Leu  
 65 70 75 80  
 Gly Cys Lys Ser Leu Arg Phe Phe Leu Glu Lys Ile Ser Phe Lys Lys  
 85 90 95  
 Arg Arg Ala Lys Ser Arg Asn Cys Asn Ile Thr Asn Val Ile Lys Ser  
 100 105 110  
 Gly Asn Glu Asp Tyr Ser Ile Phe Ile Thr Ser Gly Ala Leu Trp Arg  
 115 120 125  
 Lys Leu Leu Asn Thr Lys Arg Thr Val Trp Ile Ile Ser Leu Ala Asn  
 130 135 140  
 Asn Asp Glu Tyr Ile Lys Phe Ile Cys Glu Cys Val Lys Gly Ser Arg  
 145 150 155 160

Tyr Ile Arg Leu Thr Lys Asp Lys Leu Ala Ile Lys Arg Lys Lys Lys  
 165 170 175  
 Phe Asp Asn Arg Thr Ala Glu Glu Leu Ile Ala Phe Thr Ile Arg Met  
 180 185 190  
 Gly Phe Ile Thr Ile Val Leu Gly Ile Asp Gly Glu Leu Pro Ser Leu  
 195 200 205  
 Glu Thr Ile Glu Lys Ala Val Tyr Asn Cys Arg Asn Arg Ser Ser Glu  
 210 215 220  
 Ser Ser Asp Val Tyr Ala Ile Ile Leu Cys Ile Asn Leu Lys Tyr Leu  
 225 230 235 240  
 Ile Ser Ile Trp Ile Ala Ile Glu Thr Asn Gln Ile Asn His Ala Ser  
 245 250 255  
 Leu Met Glu Tyr Thr Leu Asn Pro Leu Gly Gln Met His Thr Glu Phe  
 260 265 270  
 Ile Leu Asp Ser Ser Ile Asp Thr Gln Asn Ala Leu Glu Thr Asp Leu  
 275 280 285  
 Ala Tyr Asn Arg Leu Pro Val Leu Ile Thr Leu Ala His Leu Leu Tyr  
 290 295 300  
 Leu Lys Lys Gln Ala Lys Cys Lys Glu Asp Arg Lys Arg Phe Gln Asn  
 305 310 315 320  
 Leu Leu Ile Leu Leu Pro Glu Leu Thr Thr Arg Ile Leu Ala Thr Lys  
 325 330 335  
 Lys Lys Lys Ser Tyr His Asn Pro Asp Ser Arg Phe Gln Lys Phe Gln  
 340 345 350  
 Val Arg Glu Ile His Ser Leu Lys Phe Ile Tyr Tyr Ser Phe Ser Phe  
 355 360 365  
 His Ser Cys Tyr Phe Leu Leu Ser Gln Tyr Phe Leu Ile Ser Trp Lys  
 370 375 380  
 Lys Val Ser Asn Lys Arg Ser Ala Arg Leu Arg Leu Ser Leu Phe Thr  
 385 390 395 400  
 Phe Ile Asp Arg Pro Ser Tyr Ile Gln Tyr Asp Asp Lys Glu Thr Ala  
 405 410 415  
 Val Ile Arg Phe Lys Asn Ser Ala Met Arg Thr Lys Phe Leu Glu Ser  
 420 425 430  
 Arg Asn Gly Ala Glu Ile Leu Ile Lys Lys Asn Cys Val Asp Ile Ala  
 435 440 445  
 Lys Glu Ser Asn Ser Lys Ser Phe Val Asn Lys Tyr Tyr Gln Ser Cys  
 450 455 460  
 Leu Ile Glu Glu Ile Asp Glu Ala Thr Ala Gln Lys Ile Ile Lys Glu  
 465 470 475 480  
 Ile Lys Leu Leu Leu Ile Arg Glu Thr Lys Leu Leu Ile Arg Ser Ala  
 485 490 495

Ile Phe Asn Cys Arg Asn Lys Ser Cys Thr Lys Val Arg Gln Lys Ile  
500 505 510

Gln Thr Leu Val Lys Ile Leu Arg Lys Glu Lys Lys Thr Ser Gln Lys  
515 520 525

Lys Lys Gly Asn Lys Asn Glu Tyr Arg Ser Glu Glu Ile Lys Asp Leu  
530 535 540

Phe Phe Ser Ile Ile Tyr Cys Lys Glu Gly Phe Trp Gly Phe Gly Val  
545 550 555 560

Leu Gly

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 560 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Lys Pro Gln Asn Pro Lys Thr Pro Ile Lys Lys Glu Lys Ile Glu  
1 5 10 15

Val Val Lys Asn Ile Ile Pro Ala Gln Met Glu Met Asp Ile Asp Leu  
20 25 30

Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn Lys Tyr Ser Ser  
35 40 45

Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys Ser Gly Ser Lys  
50 55 60

Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln Leu Glu Phe Tyr  
65 70 75 80

Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu Arg Lys Leu Val  
85 90 95

Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr Leu Leu Met Phe  
100 105 110

Lys Asn Gln Val Met Arg Ile Ile Leu Phe Phe Arg Ser Leu Leu Lys  
115 120 125

Glu His Tyr Gly Glu Asn Tyr Leu Ile Leu Lys Gly Lys Gln Phe Gly  
130 135 140

Leu Phe Pro Pro Thr Met Met Ser Ile Leu Asn Ser Tyr Glu Asn Glu  
145 150 155 160

Ser Lys Asp Leu Asp Thr Ser Asp Leu Pro Lys Thr Asn Ser Leu Asn  
165 170 175

Ala Arg Lys Ser Leu Ile Ile Glu Gln Gln Lys Asn Leu Leu His Leu  
180 185 190



Leu Phe Val Trp Val Leu Leu Gln Leu Phe Val Ser Thr Val Asn Ser  
 195 200 205  
 Arg Val Leu Arg Gln Leu Lys Lys Leu Phe Thr Thr Glu Gly Ile Ala  
 210 215 220  
 Val Leu Lys Val Leu Met Cys Met Pro Leu Phe Cys Glu Leu Ile Ser  
 225 230 235 240  
 Asn Ile Leu Ser Gln Phe Asn Gly Leu Lys Gln Thr Lys Thr Met Gln  
 245 250 255  
 Val Trp Asn Ile Arg Ile Leu Trp Asp Lys Cys Thr Leu Asn Leu Tyr  
 260 265 270  
 Trp Ile Leu Lys Ala Ile His Arg Met Leu Arg Leu Ile Leu Thr Thr  
 275 280 285  
 Asp Tyr Leu Phe Cys Leu Leu Leu Leu Ile Ser Tyr Ile Phe Lys Arg  
 290 295 300  
 Ser Arg Arg Asn Glu Lys Lys Thr Lys Glu Arg Asp Phe Lys Ile Cys  
 305 310 315 320  
 Cys Phe Phe Cys Asn Arg Asn Gln Gln Glu Tyr Gln Arg Lys Arg Arg  
 325 330 335  
 Arg Ala Ile Thr Ile Leu Ile Leu Lys Asp Phe Lys Asn Ser Arg Glu  
 340 345 350  
 Arg Tyr Ile His Asn Ser Tyr Ile Ile Val Phe His Phe Thr Ala Val  
 355 360 365  
 Ile Phe Phe Tyr Leu Asn Asn Ile Phe Cys Leu Ala Gly Ser Lys Lys  
 370 375 380  
 Tyr Gln Ile Arg Glu Ala Leu Asp Cys Gly Asn Leu Ala Tyr Ser His  
 385 390 395 400  
 Ser Ile Asp Leu His Ile Ser Asn Thr Met Ile Arg Lys Gln Gln Ser  
 405 410 415  
 Ser Val Leu Lys Ile Val Leu Cys Gly Leu Asn Phe Ser Gln Glu Met  
 420 425 430  
 Glu Pro Lys Ser Ser Lys Arg Ile Ala Ser Ile Leu Gln Lys Asn Arg  
 435 440 445  
 Thr Leu Asn Leu Ser Leu Ile Ser Ile Thr Asn Leu Asp Cys Leu Lys  
 450 455 460  
 Arg Leu Thr Arg Gln Leu His Arg Arg Ser Leu Lys Lys Ser Asn Phe  
 465 470 475 480  
 Tyr Leu Glu Asn Lys Leu Asn Tyr Tyr Arg Asp Gln Arg Ser Ser Ile  
 485 490 495  
 Asp Glu Ile Lys Ala Glu Leu Lys Leu Asp Asn Lys Lys Tyr Lys Pro  
 500 505 510  
 Trp Ser Lys Tyr Cys Gly Arg Lys Arg Arg Pro Val Ser Lys Arg Lys  
 515 520 525

Asn Lys Ala Ile Asn Lys Met Ser Thr Glu Val Lys Lys Lys Ile Tyr  
530 535 540

Phe Phe Gln Phe Ile Glu Lys Arg Gly Phe Gly Val Leu Gly Phe Trp  
545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Ile Glu Asn Asn Gln Ala Gln Gln Pro Lys Ala Glu Lys Leu  
1 5 10 15

Trp Trp Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln  
20 25 30

Val Arg Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr  
35 40 45

Ala Ala Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu  
50 55 60

Arg Arg Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp  
65 70 75 80

Pro Glu Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr  
85 90 95

Ile Arg Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys  
100 105 110

Asn Thr Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu  
115 120 125

Pro Asn Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile  
130 135 140

Phe Asp Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser  
145 150 155 160

Gln Asp Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys  
165 170 175

Val Arg Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr  
180 185 190

Cys Thr Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val  
195 200 205

Thr Asn Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn  
210 215 220

Leu Leu Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys  
225 230 235 240

Arg	Glu	Thr	Gly	Asp	Ile	Met	Asn	Val	Glu	Asp	Ala	Ile	Lys	Ala	Leu	245	250	255
Lys	Pro	Ala	Val	Met	Lys	Lys	Ile	Ala	Lys	Arg	Gln	Asn	Ala	Met	Lys	260	265	270
Lys	His	Met	Lys	Ala	Pro	Lys	Ile	Pro	Asn	Ser	Thr	Leu	Glu	Ser	Lys	275	280	285
Tyr	Leu	Thr	Phe	Lys	Asp	Leu	Ile	Lys	Phe	Cys	His	Ile	Ser	Glu	Pro	290	295	300
Lys	Glu	Arg	Val	Tyr	Lys	Ile	Leu	Gly	Lys	Lys	Tyr	Pro	Lys	Thr	Glu	305	310	315
Glu	Glu	Tyr	Lys	Ala	Ala	Phe	Gly	Asp	Ser	Ala	Ser	Ala	Pro	Phe	Asn	325	330	335
Pro	Glu	Leu	Ala	Gly	Lys	Arg	Met	Lys	Ile	Glu	Ile	Ser	Lys	Thr	Trp	340	345	350
Glu	Asn	Glu	Leu	Ser	Ala	Lys	Gly	Asn	Thr	Ala	Glu	Val	Trp	Asp	Asn	355	360	365
Leu	Ile	Ser	Ser	Asn	Gln	Leu	Pro	Tyr	Met	Ala	Met	Leu	Arg	Asn	Leu	370	375	380
Ser	Asn	Ile	Leu	Lys	Ala	Gly	Val	Ser	Asp	Thr	Thr	His	Ser	Ile	Val	385	390	395
Ile	Asn	Lys	Ile	Cys	Glu	Pro	Lys	Ala	Val	Glu	Asn	Ser	Lys	Met	Phe	405	410	415
Pro	Leu	Gln	Phe	Phe	Ser	Ala	Ile	Glu	Ala	Val	Asn	Glu	Ala	Val	Thr	420	425	430
Lys	Gly	Phe	Lys	Ala	Lys	Lys	Arg	Glu	Asn	Met	Asn	Leu	Lys	Gly	Gln	435	440	445
Ile	Glu	Ala	Val	Lys	Glu	Val	Val	Glu	Lys	Thr	Asp	Glu	Glu	Lys	Lys	450	455	460
Asp	Met	Glu	Leu	Glu	Gln	Thr	Glu	Glu	Gly	Glu	Phe	Val	Lys	Val	Asn	465	470	475
Glu	Gly	Ile	Gly	Lys	Gln	Tyr	Ile	Asn	Ser	Ile	Glu	Leu	Ala	Ile	Lys	485	490	495
Ile	Ala	Val	Asn	Lys	Asn	Leu	Asp	Glu	Ile	Lys	Gly	His	Thr	Ala	Ile	500	505	510
Phe	Ser	Asp	Val	Ser	Gly	Ser	Met	Ser	Thr	Ser	Met	Ser	Gly	Gly	Ala	515	520	525
Lys	Lys	Tyr	Gly	Ser	Val	Arg	Thr	Cys	Leu	Glu	Cys	Ala	Leu	Val	Leu	530	535	540
Gly	Leu	Met	Val	Lys	Gln	Arg	Cys	Glu	Lys	Ser	Ser	Phe	Tyr	Ile	Phe	545	550	555
Ser	Ser	Pro	Ser	Ser	Gln	Cys	Asn	Lys	Cys	Tyr	Leu	Glu	Val	Asp	Leu	565	570	575



Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp  
130 135 140

Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg  
145 150 155 160

Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln  
165 170 175

Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp  
180 185 190

Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val  
195 200 205

Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp  
210 215 220

Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn  
225 230 235 240

Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg  
245 250 255

Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser  
260 265 270

Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu  
275 280 285

Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His  
290 295 300

Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser  
305 310 315 320

Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr  
325 330 335

Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe  
340 345 350

Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro  
355 360 365

Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys  
370 375 380

Val Lys His Ala Asn Leu Asn Leu Val Ser Ile Pro Thr Gln Phe Asn  
385 390 395 400

Phe Asp Phe Tyr Phe Val Asn Leu Gln His Leu Lys Leu Glu Phe Gly  
405 410 415

Leu Glu Pro Asn Ile Leu Thr Lys Gln Lys Leu Glu Asn Leu Leu Leu  
420 425 430

Ser Ile Lys Gln Ser Lys Asn Leu Lys Phe Leu Arg Leu Asn Phe Tyr  
435 440 445

Thr Tyr Val Ala Gln Glu Thr Ser Arg Lys Gln Ile Leu Lys Gln Ala  
450 455 460

Thr	Thr	Ile	Lys	Asn	Leu	Lys	Asn	Asn	Lys	Asn	Gln	Glu	Glu	Thr	Pro	465	470	475	480
Glu	Thr	Lys	Asp	Glu	Thr	Pro	Ser	Glu	Ser	Thr	Ser	Gly	Met	Lys	Phe	485	490	495	
Phe	Asp	His	Leu	Ser	Glu	Leu	Thr	Glu	Leu	Glu	Asp	Phe	Ser	Val	Asn	500	505	510	
Leu	Gln	Ala	Thr	Gln	Glu	Ile	Tyr	Asp	Ser	Leu	His	Lys	Leu	Leu	Ile	515	520	525	
Arg	Ser	Thr	Asn	Leu	Lys	Lys	Phe	Lys	Leu	Ser	Tyr	Lys	Tyr	Glu	Met	530	535	540	
Glu	Lys	Ser	Lys	Met	Asp	Thr	Phe	Ile	Asp	Leu	Lys	Asn	Ile	Tyr	Glu	545	550	555	560
Thr	Leu	Asn	Asn	Leu	Lys	Arg	Cys	Ser	Val	Asn	Ile	Ser	Asn	Pro	His	565	570	575	
Gly	Asn	Ile	Ser	Tyr	Glu	Leu	Thr	Asn	Lys	Asp	Ser	Thr	Phe	Tyr	Lys	580	585	590	
Phe	Lys	Leu	Thr	Leu	Asn	Gln	Glu	Leu	Gln	His	Ala	Lys	Tyr	Thr	Phe	595	600	605	
Lys	Gln	Asn	Glu	Phe	Gln	Phe	Asn	Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu	610	615	620	
Ser	Ser	Ser	Leu	Glu	Ser	Leu	Glu	Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser	625	630	635	640
Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln	Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	645	650	655	
Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys	Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	660	665	670	
Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln	Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	675	680	685	
Ile	Asn	Cys	Ile	Leu	Asp	Gln	His	Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	690	695	700	
Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys	Ala	Phe	Ile	Leu	Lys	Arg	Tyr	Tyr	705	710	715	720
Leu	Leu	Gln	Tyr	Tyr	Leu	Asp	Tyr	Thr	Lys	Leu	Phe	Lys	Thr	Leu	Gln	725	730	735	
Gln	Leu	Pro	Glu	Leu	Asn	Gln	Val	Tyr	Ile	Asn	Gln	Gln	Leu	Glu	Glu	740	745	750	
Leu	Thr	Val	Ser	Glu	Val	His	Lys	Gln	Val	Trp	Glu	Asn	His	Lys	Gln	755	760	765	
Lys	Ala	Phe	Tyr	Glu	Pro	Leu	Cys	Glu	Phe	Ile	Lys	Glu	Ser	Ser	Gln	770	775	780	
Thr	Leu	Gln	Leu	Ile	Asp	Phe	Asp	Gln	Asn	Thr	Val	Ser	Asp	Asp	Ser	785	790	795	800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
805 810 815

Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu  
835 840 845

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr  
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp  
865 870

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn Thr Phe Asn  
1 5 10 15

Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys Thr Leu Lys  
20 25 30

Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu Gln Lys Gln  
35 40 45

Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp Ser Phe Leu  
50 55 60

Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu Ile Glu Thr  
65 70 75 80

Leu Leu Met

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn Val Lys Ser Ala Lys Ile Glu Ser Ser Ser Leu Glu Ser Leu Glu  
1 5 10 15

Asp Ile Asp Ser Leu Cys Lys Ser Ile Ala Ser Cys Lys Asn Leu Gln  
20 25 30

Asn Val Asn Ile Ile Ala Ser Leu Leu Tyr Pro Asn Asn Ile Gln Lys  
35 40 45

Asn Pro Phe Asn Lys Pro Asn Leu Leu Phe Phe Lys Gln Phe Glu Gln  
50 55 60

Leu Lys Asn Leu Glu Asn Val Ser Ile Asn Cys Ile Leu Asp Gln His  
65 70 75 80

Ile Leu Asn Ser Ile Ser Glu Phe Leu Glu Lys Asn Lys Lys Ile Lys  
85 90 95

Ala Phe Ile Leu  
100

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Met Asp Ile Asp Leu Asp Asp Ile Glu Asn Leu Leu Pro Asn  
1 5 10 15

Thr Phe Asn Lys Tyr Ser Ser Ser Cys Ser Asp Lys Lys Gly Cys Lys  
20 25 30

Thr Leu Lys Ser Gly Ser Lys Ser Pro Ser Leu Thr Ile Pro Lys Leu  
35 40 45

Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn Asp  
50 55 60

Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val Glu  
65 70 75 80

Ile Glu Thr Leu Leu  
85

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Glu Leu Ala Ile Lys Ile Ala Val Asn Lys Asn Leu Asp Glu Ile  
1 5 10 15

Lys Gly His Thr Ala Ile Phe Ser Asp Val Ser Gly Ser Met Ser Thr  
20 25 30



Ser Met Ser Gly Gly Ala Lys Lys Tyr Gly Ser Val Arg Thr Cys Leu  
35 40 45  
Glu Cys Ala Leu Val Leu Gly Leu Met Val Lys Gln Arg Cys Glu Lys  
50 55 60  
Ser Ser Phe Tyr Ile Phe Ser Ser Pro Ser Ser Gln Cys Lys Cys Tyr  
65 70 75 80  
Leu Glu Val Asp Leu Pro Gly Asp Glu Leu Arg Pro Ser Met Gln Lys  
85 90 95  
Leu Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr  
1 5 10 15  
Asp Ser Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys Thr Thr Lys  
20 25 30  
Leu Leu Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys  
35 40 45  
Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser  
50 55 60  
Ser Leu Gly Phe Leu  
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Asn Arg Asn Leu His Cys Thr Tyr Ile Asp Tyr Lys Lys Ala Phe  
1 5 10 15  
Asp Ser Ile Pro His Ser Trp Leu Ile Gln Val Leu Glu Ile Tyr Lys  
20 25 30  
Ile Asn Arg Gln Ile Ala Ile Lys Lys Gly Ile Tyr Gln Gly Asp Ser  
35 40 45

Leu Ser Pro Leu Trp Phe Cys Leu Ala Leu Asn Pro Leu Ser His Gln  
50 55 60

Leu His Asn Asp Arg  
65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Gly Gly Ser Asn Trp Phe Arg Glu Val Asp Leu Lys Lys Cys Phe  
1 5 10 15

Asp Thr Ile Ser His Asp Leu Ile Ile Lys Glu Leu Lys Arg Tyr Ile  
20 25 30

Ser Asp His Val Pro Val Gly Pro Arg Val Cys Val Gln Gly Ala Pro  
35 40 45

Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu Asp Arg Arg  
50 55 60

Leu Ala Gly Leu Ala  
65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr  
1 5 10 15

Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr  
20 25 30

Ile Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys  
35 40 45

Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro  
50 55 60

Phe Arg Lys Gln Asn  
65

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Leu Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr  
1 5 10 15  
Asp Ser Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys Asp Ala Leu  
20 25 30  
Lys Asn Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser  
35 40 45  
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe  
50 55 60  
Tyr Ser Glu Phe Lys  
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu Asn  
1 5 10 15  
Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu Asn  
20 25 30  
Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Gln Asp Tyr Cys Asp  
35 40 45  
Trp Ile Gly Ile Ser Ile  
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

His Leu Ile Tyr Met Asp Asp Ile Lys Leu Tyr Ala Lys Asn Asp Lys  
1 5 10 15  
Glu Met Lys Lys Leu Ile Asp Thr Thr Thr Ile Phe Ser Asn Asp Ile  
20 25 30  
Ser Met Gln Phe Gly Leu Asp Lys Cys Lys Thr Lys Cys Leu Tyr Lys  
35 40 45  
Tyr Leu Gly Phe Gln Gln  
50

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Arg Tyr Ala Asp Asp Ile Leu Ile Gly Val Leu Gly Ser Lys  
1 5 10 15  
Asn Lys Ile Ile Lys Arg Asp Leu Asn Asn Phe Leu Asn Ser Leu Gly  
20 25 30  
Leu Thr Ile Asn Glu Glu Lys Thr Leu Ile Glu Thr Pro Ala Arg Phe  
35 40 45  
Leu Gly Tyr Asn Ile  
50

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser His Leu Glu Ile  
1 5 10 15  
Gly His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp  
20 25 30  
Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu  
35 40 45  
Trp Met Gly Tyr Glu Leu  
50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln Gln  
1 5 10 15  
Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr  
20 25 30  
Asn Ala Lys Ala Asn Arg Ile Arg Ser Lys Ser Ser Lys Gly Ile Phe  
35 40 45  
Arg

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Gln Lys Gln Leu Glu Phe Tyr Phe Ser Asp Ala Asn Leu Tyr Asn  
1 5 10 15  
Asp Ser Phe Leu Arg Lys Leu Val Leu Lys Ser Gly Glu Gln Arg Val  
20 25 30  
Glu Ile Glu Thr Leu Leu Met  
35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile Cys His Gln Glu Tyr Tyr Phe Gly Asp Phe Asn Leu Pro Arg Asp  
1 5 10 15  
Lys Phe Leu Lys Glu Gln Ile Lys Leu Asp Glu Gly Trp Val Pro Leu  
20 25 30  
Glu Ile Met Ile Lys  
35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Cys Glu Gln Ile Glu Tyr Tyr Phe Gly Asp His Asn Leu Pro Arg  
1 5 10 15  
Asp Lys Phe Leu Lys Gln Gln Ile Leu Leu Asp Asp Gly Trp Val Pro  
20 25 30  
Leu Glu Thr Met Ile Lys  
35

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile Leu Arg Gln Val Glu Tyr Tyr Phe Gly Asp Ala Asn Leu Asn Arg  
1 5 10 15  
Asp Lys Phe Leu Arg Glu Gln Ile Gly Lys Asn Glu Asp Gly Trp Val  
20 25 30  
Pro Leu Ser Val Leu Val Thr  
35

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Leu Lys Gln Val Glu Phe Tyr Phe Ser Glu Phe Asn Phe Pro Tyr  
1 5 10 15  
Asp Arg Phe Leu Arg Thr Thr Ala Glu Lys Asn Asp Gly Trp Val Pro  
20 25 30  
Ile Ser Thr Ile Ala Thr  
35

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TAGACCTGTT AGTGTTACATT TGAATTGAAG C

31

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TAGACCTGTT AGGTTGGATT TGTGGCATCA

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAAAACCCCA AAACCTAACA GGTCTA

26

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCGGGAATTC TAATACGACT CACTATAGGG AAGAACTCT GATGAGGCCG AAAGGCCGAA 60

ACTCCACGAA AGTGGAGTAA GTTCTCGAT AATTGATCTG TAG 103

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGATCCT CTTCAAAGA TGAGAGGACA GCAAAC 36

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCAAAACC CAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTTGGGG 60

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAAAACCCC AAAACCCCCA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTTGGGG 58



(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TTGGGG

56

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AACCCCAAAA CCCCAAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT GGGG

54

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 48 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCCCAAAACC CCAAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAAACCCCAA AACCCCAAAA CCCCCACAGG GGTTTTGGGG TTTTGGGGTT TT

52

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACCCCAAAA CCCCAAACC CCCACAGGGG TTTTGGGGTT TTGGGGTTTT

50

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCCCAAAACC CCAAACCCC CACAGGGGTT TTGGGGTTTT GGGGTTTT

48

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCAAAACCCC AAAACCCCCA CAGGGGTTTT GGGGTTTTGG GGTTTT

46

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAAACCCCAA AACCCCCACA GGGGTTTTGG GGTTTTGGGG TTTT

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTGGGG

8

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "RNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAAAACCCCA AAACC

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGGGTTTT

8

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCTRAARTAR TGDGTNADRT TRTTCAT

27

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCGGATCCAT GAAYCCWGAR AAYCCWAAYG T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

NNNGTNACHG GHATHAAYAA

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

DGCDGTYTCY TGRTCRTRT A

21

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AACTCATTTA ATTACTAATT TAATCAACAA GATTGATAAA AAGCAGTAAA TAAAACCCAA	60
TAGATTTAAT TTAGAAAGTA TCAATTGAAA AATGGAAATT GAAAACAACT AAGCACAATA	120
GCCAAAAGCC GAAAAATTGT GGTGGGAACT TGAATTAGAG ATGCAAGAAA ACCAAAATGA	180
TATATAAGTT AGGGTTAAGA TTGACGATCC TAAGCAATAT CTCGTGAACG TCACTGCAGC	240
ATGTTTGTG TAGGAAGGTA GTTACTACTA AGATAAGAT GAAAGAAGAT ATATCATCAC	300
TAAAGCACTT CTTGAGGTGG CTGAGTCTGA TCCTGAGTTC ATCTGCTAGT TGGCAGTCTA	360
CATCCGTAAT GAACTTTACA TCAGAACTAC CACTAACTAC ATTGTAGCAT TTTGTGTTGT	420
CCACAAGAAT ACTCAACCAT TCATCGAAAA GTACTTCAAC AAAGCAGTAC TTTTGCCTAA	480
TGACTTACTG GAAGTCTGTG AATTTCGATA GGTTCCTCTAT ATTTTGTATG CAACTGAATT	540
CAAAAATTTG TATCTTGATA GGATACTTTC ATAAGATATT CGTAAGGAAC TCACTTTCCG	600
TAAGTGTTTA CAAAGATGCG TCAGAAGCAA GTTTTCTGAA TTCAACGAAT ACTAACTTGG	660
TAAGTATTGC ACTGAATCCT AACGTAAGAA AACAATGTTC CGTTACCTCT CAGTTACCAA	720
CAAGTAAAG TGGGATTAAA CTAAGAAGAA GAGAAAAGAG AATCTCTTAA CCAAACTTTA	780
GGCAATAAAG GAATCTGAAG ATAAGTCCAA GAGAGAACT GGAGACATAA TGAACGTTGA	840
AGATGCAATC AAGGCTTTAA AACCAGCAGT TATGAAGAAA ATAGCCAAGA GATAGAATGC	900
CATGAAGAAA CACATGAAGG CACCTAAAAT TCCTAACTCT ACCTTGGAAT CAAAGTACTT	960
GACCTTCAAG GATCTCATT AGTTCTGCCA TATTTCTGAG CCTAAAGAAA GAGTCTATAA	1020
GATCCTTGGT AAAAAATACC CTAAGACCGA AGAGGAATAC AAAGCAGCCT TTGGTGATTC	1080
TGCATCTGCA CCCTTCAATC CTGAATTGGC TGGAAAGCGT ATGAAGATTG AAATCTCTAA	1140
AACATGGGAA AATGAACTCA GTGCAAAAGG CAACACTGCT GAGGTTTGGG ATAATTTAAT	1200
TTCAAGCAAT TAACTCCCAT ATATGGCCAT GTTACGTAAC TTGTCTAACA TCTTAAAAGC	1260
CGGTGTTTCA GATACTACAC ACTCTATTGT GATCAACAAG ATTTGTGAGC CCAAGGCCGT	1320
TGAGAACTCC AAGATGTTCC CTCTTCAATT CTTTAGTGCC ATTGAAGCTG TTAATGAAGC	1380
AGTTACTAAG GGATTCAAGG CCAAGAAGAG AGAAAATATG AATCTTAAAG GTCAAATCGA	1440
AGCAGTAAAG GAAGTTGTTG AAAAAACCGA TGAAGAGAAG AAAGATATGG AGTTGGAGTA	1500

AACCGAAGAA GGAGAATTTG TTAAAGTCAA CGAAGGAATT GGCAAGCAAT ACATTAACTC 1560  
 CATTGAACTT GCAATCAAGA TAGCAGTTAA CAAGAATTTA GATGAAATCA AAGGACACAC 1620  
 TGCAATCTTC TCTGATGTTT CTGGTTCTAT GAGTACCTCA ATGTCAGGTG GAGCCAAGAA 1680  
 GTATGGTTCC GTTCGTACTT GTCTCGAGTG TGCATTAGTC CTTGGTTTGA TGGTAAAATA 1740  
 ACGTTGTGAA AAGTCCTCAT TCTACATCTT CAGTTCACCT AGTTCTCAAT GCAATAAGTG 1800  
 TTAAGTAGAA GTTGATCTCC CTGGAGACGA ACTCCGTCCT TCTATGTAAA AACTTTTGCA 1860  
 AGAGAAAGGA AAAGTTGGTG GTGGTACTGA TTTCCCCTAT GAGTGCATTG ATGAATGGAC 1920  
 AAAGAATAAA ACTCACGTAG ACAATATCGT TATTTTGTCT GATATGATGA TTGCAGAAGG 1980  
 ATATTCAGAT ATCAATGTTA GAGGCAGTTC CATTGTTAAC AGCATCAAAA AGTACAAGGA 2040  
 TGAAGTAAAT CCTAACATTA AAATCTTTGC AGTTGACTTA GAAGGTTACG GAAAGTGCCT 2100  
 TAATCTAGGT GATGAGTTCA ATGAAAACAA CTACATCAAG ATATTCGGTA TGAGCGATTG 2160  
 AATCTTAAAG TTCATTTTCA CCAAGCAAGG AGGAGCAAAT ATGGTCGAAG TTATCAAAAA 2220  
 CTTTGCCCTT CAAAAAATAG GACAAAAGTG AGTTTCTTGA GATTCTTCTA TAACAAAAAT 2280  
 CTCACCCAC TTTTTTGTTC TATTGCATAG CCATTATGAA ATTTAAATTA TTATCTATTT 2340  
 ATTTAAGTTA CTTACATAGT TTATGTATCG CAGTCTATTA GCCTATTCAA ATGATTCTGC 2400  
 AAAGAACAAA AAAGATTAAA A 2421

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Glu Leu Glu Leu Glu Met Gln Glu Asn Gln Asn Asp Ile Gln Val Arg  
 1 5 10 15  
 Val Lys Ile Asp Asp Pro Lys Gln Tyr Leu Val Asn Val Thr Ala Ala  
 20 25 30  
 Cys Leu Leu Gln Glu Gly Ser Tyr Tyr Gln Asp Lys Asp Glu Arg Arg  
 35 40 45  
 Tyr Ile Ile Thr Lys Ala Leu Leu Glu Val Ala Glu Ser Asp Pro Glu  
 50 55 60  
 Phe Ile Cys Gln Leu Ala Val Tyr Ile Arg Asn Glu Leu Tyr Ile Arg  
 65 70 75 80  
 Thr Thr Thr Asn Tyr Ile Val Ala Phe Cys Val Val His Lys Asn Thr  
 85 90 95

Gln Pro Phe Ile Glu Lys Tyr Phe Asn Lys Ala Val Leu Leu Pro Asn  
100 105 110

Asp Leu Leu Glu Val Cys Glu Phe Ala Gln Val Leu Tyr Ile Phe Asp  
115 120 125

Ala Thr Glu Phe Lys Asn Leu Tyr Leu Asp Arg Ile Leu Ser Gln Asp  
130 135 140

Ile Arg Lys Glu Leu Thr Phe Arg Lys Cys Leu Gln Arg Cys Val Arg  
145 150 155 160

Ser Lys Phe Ser Glu Phe Asn Glu Tyr Gln Leu Gly Lys Tyr Cys Thr  
165 170 175

Glu Ser Gln Arg Lys Lys Thr Met Phe Arg Tyr Leu Ser Val Thr Asn  
180 185 190

Lys Gln Lys Trp Asp Gln Thr Lys Lys Lys Arg Lys Glu Asn Leu Leu  
195 200 205

Thr Lys Leu Gln Ala Ile Lys Glu Ser Glu Asp Lys Ser Lys Arg Glu  
210 215 220

Thr Gly Asp Ile Met Asn Val Glu Asp Ala Ile Lys Ala Leu Lys Pro  
225 230 235 240

Ala Val Met Lys Lys Ile Ala Lys Arg Gln Asn Ala Met Lys Lys His  
245 250 255

Met Lys Ala Pro Lys Ile Pro Asn Ser Thr Leu Glu Ser Lys Tyr Leu  
260 265 270

Thr Phe Lys Asp Leu Ile Lys Phe Cys His Ile Ser Glu Pro Lys Glu  
275 280 285

Arg Val Tyr Lys Ile Leu Gly Lys Lys Tyr Pro Lys Thr Glu Glu Glu  
290 295 300

Tyr Lys Ala Ala Phe Gly Asp Ser Ala Ser Ala Pro Phe Asn Pro Glu  
305 310 315 320

Leu Ala Gly Lys Arg Met Lys Ile Glu Ile Ser Lys Thr Trp Glu Asn  
325 330 335

Glu Leu Ser Ala Lys Gly Asn Thr Ala Glu Val Trp Asp Asn Leu Ile  
340 345 350

Ser Ser Asn Gln Leu Pro Tyr Met Ala Met Leu Arg Asn Leu Ser Asn  
355 360 365

Ile Leu Lys Ala Gly Val Ser Asp Thr Thr His Ser Ile Val Ile Asn  
370 375 380

Lys Ile Cys Glu Pro Lys Ala Val Glu Asn Ser Lys Met Phe Pro Leu  
385 390 395 400

Gln Phe Phe Ser Ala Ile Glu Ala Val Asn Glu Ala Val Thr Lys Gly  
405 410 415

Phe Lys Ala Lys Lys Arg Glu Asn Met Asn Leu Lys Gly Gln Ile Glu  
420 425 430

Ala Val Lys Glu Val Val Glu Lys Thr Asp Glu Glu Lys Lys Asp Met  
435 440 445

Glu Leu Glu Gln Thr Glu Glu Gly Glu Phe Val Lys Val Asn Glu Gly  
450 455 460

Ile Gly Lys Gln Tyr Ile Asn Ser Ile Glu Leu Ala Ile Lys Ile Ala  
465 470 475 480

Val Asn Lys Asn Leu Asp Glu Ile Lys Gly His Thr Ala Ile Phe Ser  
485 490 495

Asp Val Ser Gly Ser Met Ser Thr Ser Met Ser Gly Gly Ala Lys Lys  
500 505 510

Tyr Gly Ser Val Arg Thr Cys Leu Glu Cys Ala Leu Val Leu Gly Leu  
515 520 525

Met Val Lys Gln Arg Cys Glu Lys Ser Ser Phe Tyr Ile Phe Ser Ser  
530 535 540

Pro Ser Ser Gln Cys Asn Lys Cys Tyr Leu Glu Val Asp Leu Pro Gly  
545 550 555 560

Asp Glu Leu Arg Pro Ser Met Gln Lys Leu Leu Gln Glu Lys Gly Lys  
565 570 575

Leu Gly Gly Gly Thr Asp Phe Pro Tyr Glu Cys Ile Asp Glu Trp Thr  
580 585 590

Lys Asn Lys Thr His Val Asp Asn Ile Val Ile Leu Ser Asp Met Met  
595 600 605

Ile Ala Glu Gly Tyr Ser Asp Ile Asn Val Arg Gly Ser Ser Ile Val  
610 615 620

Asn Ser Ile Lys Lys Tyr Lys Asp Glu Val Asn Pro Asn Ile Lys Ile  
625 630 635 640

Phe Ala Val Asp Leu Glu Gly Tyr Gly Lys Cys Leu Asn Leu Gly Asp  
645 650 655

Glu Phe Asn Glu Asn Asn Tyr Ile Lys Ile Phe Gly Met Ser Asp Ser  
660 665 670

Ile Leu Lys Phe Ile Ser Ala Lys Gln Gly Gly Ala Asn Met Val Glu  
675 680 685

Val Ile Lys Asn Phe Ala Leu Gln Lys Ile Gly  
690 695

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2829 base pairs



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCAATACTAT TAATTAATAA ATAAAAAAAA GCAAACTACA AAGAAAATGT CAAGGCGTAA	60
CTAAAAAAG CCATAGGCTC CTATAGGCAA TGAAACAAAT CTTGATTTTG TATTACAAAA	120
TCTAGAAGTT TACAAAAGCC AGATTGAGCA TTATAAGACC TAGTAGTAAT AGATCAAAGA	180
GGAGGATCTC AAGCTTTTAA AGTTCAAAAA TTAAGATTAG GATGGAAACT CTGGCAACGA	240
TGATGATGAT GAAGAAAACA ACTCAAATAA ATAATAAGAA TTATTAAGGA GAGTCAATTA	300
GATTAAGTAG CAAGTTTAAAT TGATAAAAAA AGTTGGTTCT AAGGTAGAGA AAGATTTGAA	360
TTTGAACGAA GATGAAAACA AAAAGAATGG ACTTTCTGAA TAGCAAGTGA AAGAAGAGTA	420
ATTAAGAACG ATTACTGAAG AATAGGTAA GTATTAAAT TTAGTATTTA ACATGGACTA	480
CCAGTTAGAT TTAAATGAGA GTGGTGGCCA TAGAAGACAC AGAAGAGAAA CAGATTATGA	540
TACTGAAAAA TGGTTTGAAA TATCTCATGA CAAAAAAAT TATGTATCAA TTTACGCCAA	600
CTAAAAGACA TCATATTGTT GGTGGCTTAA AGATTATTTT AATAAAAACA ATTATGATCA	660
TCTTAATGTA AGCATTAACA GACTAGAAAC TGAAGCCGAA TTCTATGCCT TTGATGATTT	720
TTCAAAAACA ATCAAACCTTA CTAATAATTC TTACTAGACT GTTAACATAG ACGTTAATTT	780
TGATAATAAT CTCTGTATAC TCGCATTGCT TAGATTTTTA TTATCACTAG AAAGATTCAA	840
TATTTTGAAT ATAAGATCTT CTTATACAAG AAATTAATAT AATTTTGAGA AAATTGGTGA	900
GCTACTTGAA ACTATCTTCG CAGTTGTCTT TTCTCATCGC CACTTACAAG GCATTCATTT	960
ACAAGTTCCT TGCGAAGCGT TCTAATATTT AGTTAACTCC TCATCATAAA TTAGCGTTAA	1020
AGATAGCTAA TTATAGGTAT ACTCTTCTC TACAGACTTA AAATTAGTTG AACTAACAA	1080
AGTCCAAGAT TATTTTAAGT TCTTATAAGA ATTCCCTCGT TTGACTCATG TAAGCTAGTA	1140
GGCTATCCCA GTTAGTGCTA CTAACGCTGT AGAGAACCTC AATGTTTTAC TTAAAAGGT	1200
CAAGCATGCT AATCTTAATT TAGTTTCTAT CCCTACCTAA TTCAATTTTG ATTTCTACTT	1260
TGTTAATTTA TAACATTTGA AATTAGAGTT TGGATTAGAA CCAAATATTT TGACAAAACA	1320
AAAGCTTGAA AATCTACTTT TGAGTATAAA ATAATCAAAA AATCTTAAAT TTTTAAGATT	1380
AAACTTTTAC ACCTACGTTG CTTAAGAAAC CTCCAGAAAA CAGATATTAA AACAAGCTAC	1440
AACAATCAAA AATCTCAAAA ACAATAAAAA TCAAGAAGAA ACTCCTGAAA CTAAAGATGA	1500
AACTCCAAGC GAAAGCACAA GTGGTATGAA ATTTTTTGAT CATCTTCTG AATTAACCGA	1560
GCTTGAAGAT TTCAGCGTTA ACTTGTAAGC TACCCAAGAA ATTTATGATA GCTTGCACAA	1620

ACTTTTGATT AGATCAACAA ATTTAAAGAA GTTCAAATTA AGTTACAAAT ATGAAATGGA 1680  
AAAGAGTAAA ATGGATACAT TCATAGATCT TAAGAATATT TATGAAACCT TAAACAATCT 1740  
TAAAAGATGC TCTGTTAATA TATCAAATCC TCATGGAAAC ATTTCTTATG AACTGACAAA 1800  
TAAAGATTCT ACTTTTTATA AATTTAAGCT GACCTTAAAC TAAGAATTAT AACACGCTAA 1860  
GTATACTTTT AAGTAGAACG AATTTTAATT TAATAACGTT AAAAGTGCAA AAATTGAATC 1920  
TTCCTCATTG GAAAGCTTAG AAGATATTGA TAGTCTTTGC AAATCTATTG CTTCTTGTA 1980  
AAATTTACAA AATGTTAATA TTATCGCCAG TTTGCTCTAT CCCAACAATA TTTAGAAAAA 2040  
TCCTTTCAAT AAGCCCAATC TTCTATTTTT CAAGCAATTT GAATAATTGA AAAATTTGGA 2100  
AAATGTATCT ATCAACTGTA TTCTTGATCA GCATATACTT AATTCTATTT CAGAATTCTT 2160  
AGAAAAGAAT AAAAAAATAA AAGCATTCAT TTTGAAAAGA TATTATTTAT TACAATATTA 2220  
TCTTGATTAT ACTAAATTAT TTAAAACACT TCAATAGTTA CCTGAATTAA ATTAAGTTTA 2280  
CATTAAATTAG CAATTAGAAG AATTGACTGT GAGTGAAGTA CATAAGTAAG TATGGGAAAA 2340  
CCACAAGCAA AAAGCTTTCT ATGAACCATT ATGTGAGTTT ATCAAAGAAT CATCCTAAAC 2400  
CCTTTAGCTA ATAGATTTTG ACCAAAACAC TGTAAGTGAT GACTCTATTA AAAAGATTTT 2460  
AGAATCTATA TCTGAGTCTA AGTATCATCA TTATTTGAGA TTGAACCCTA GTTAATCTAG 2520  
CAGTTTAATT AAATCTGAAA ACGAAGAAAT TTAAGAACTT CTCAAAGCTT GCGACGAAAA 2580  
AGGTGTTTTA GTAAAAGCAT ACTATAAATT CCCTCTATGT TTACCAACTG GTACTTATTA 2640  
CGATTACAAT TCAGATAGAT GGTGATTAAT TAAATATTAG TTTAAATAAA TATTAAATAT 2700  
TGAATATTTT TTTGCTTATT ATTGAATAA TACATACAAT AGTCATTTTT AGTGTTTTGA 2760  
ATATATTTTA GTTATTTAAT TCATTATTTT AAGTAAATAA TTATTTTTC AATCATTTTTT 2820  
AAAAAATCG 2829

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Ser Arg Arg Asn Gln Lys Lys Pro Gln Ala Pro Ile Gly Asn Glu  
1 5 10 15  
Thr Asn Leu Asp Phe Val Leu Gln Asn Leu Glu Val Tyr Lys Ser Gln  
20 25 30  
Ile Glu His Tyr Lys Thr Gln Gln Gln Gln Ile Lys Glu Glu Asp Leu  
35 40 45

Lys Leu Leu Lys Phe Lys Asn Gln Asp Gln Asp Gly Asn Ser Gly Asn  
 50 55 60  
 Asp Asp Asp Asp Glu Glu Asn Asn Ser Asn Lys Gln Gln Glu Leu Leu  
 65 70 75 80  
 Arg Arg Val Asn Gln Ile Lys Gln Gln Val Gln Leu Ile Lys Lys Val  
 85 90 95  
 Gly Ser Lys Val Glu Lys Asp Leu Asn Leu Asn Glu Asp Glu Asn Lys  
 100 105 110  
 Lys Asn Gly Leu Ser Glu Gln Gln Val Lys Glu Glu Gln Leu Arg Thr  
 115 120 125  
 Ile Thr Glu Glu Gln Val Lys Tyr Gln Asn Leu Val Phe Asn Met Asp  
 130 135 140  
 Tyr Gln Leu Asp Leu Asn Glu Ser Gly Gly His Arg Arg His Arg Arg  
 145 150 155 160  
 Glu Thr Asp Tyr Asp Thr Glu Lys Trp Phe Glu Ile Ser His Asp Gln  
 165 170 175  
 Lys Asn Tyr Val Ser Ile Tyr Ala Asn Gln Lys Thr Ser Tyr Cys Trp  
 180 185 190  
 Trp Leu Lys Asp Tyr Phe Asn Lys Asn Asn Tyr Asp His Leu Asn Val  
 195 200 205  
 Ser Ile Asn Arg Leu Glu Thr Glu Ala Glu Phe Tyr Ala Phe Asp Asp  
 210 215 220  
 Phe Ser Gln Thr Ile Lys Leu Thr Asn Asn Ser Tyr Gln Thr Val Asn  
 225 230 235 240  
 Ile Asp Val Asn Phe Asp Asn Asn Leu Cys Ile Leu Ala Leu Leu Arg  
 245 250 255  
 Phe Leu Leu Ser Leu Glu Arg Phe Asn Ile Leu Asn Ile Arg Ser Ser  
 260 265 270  
 Tyr Thr Arg Asn Gln Tyr Asn Phe Glu Lys Ile Gly Glu Leu Leu Glu  
 275 280 285  
 Thr Ile Phe Ala Val Val Phe Ser His Arg His Leu Gln Gly Ile His  
 290 295 300  
 Leu Gln Val Pro Cys Glu Ala Phe Gln Tyr Leu Val Asn Ser Ser Ser  
 305 310 315 320  
 Gln Ile Ser Val Lys Asp Ser Gln Leu Gln Val Tyr Ser Phe Ser Thr  
 325 330 335  
 Asp Leu Lys Leu Val Asp Thr Asn Lys Val Gln Asp Tyr Phe Lys Phe  
 340 345 350  
 Leu Gln Glu Phe Pro Arg Leu Thr His Val Ser Gln Gln Ala Ile Pro  
 355 360 365  
 Val Ser Ala Thr Asn Ala Val Glu Asn Leu Asn Val Leu Leu Lys Lys  
 370 375 380

Val	Lys	His	Ala	Asn	Leu	Asn	Leu	Val	Ser	Ile	Pro	Thr	Gln	Phe	Asn	
385					390					395					400	
Phe	Asp	Phe	Tyr	Phe	Val	Asn	Leu	Gln	His	Leu	Lys	Leu	Glu	Phe	Gly	
				405					410					415		
Leu	Glu	Pro	Asn	Ile	Leu	Thr	Lys	Gln	Lys	Leu	Glu	Asn	Leu	Leu	Leu	
			420					425					430			
Ser	Ile	Lys	Gln	Ser	Lys	Asn	Leu	Lys	Phe	Leu	Arg	Leu	Asn	Phe	Tyr	
		435					440					445				
Thr	Tyr	Val	Ala	Gln	Glu	Thr	Ser	Arg	Lys	Gln	Ile	Leu	Lys	Gln	Ala	
	450					455					460					
Thr	Thr	Ile	Lys	Asn	Leu	Lys	Asn	Asn	Lys	Asn	Gln	Glu	Glu	Thr	Pro	
465					470					475					480	
Glu	Thr	Lys	Asp	Glu	Thr	Pro	Ser	Glu	Ser	Thr	Ser	Gly	Met	Lys	Phe	
			485						490					495		
Phe	Asp	His	Leu	Ser	Glu	Leu	Thr	Glu	Leu	Glu	Asp	Phe	Ser	Val	Asn	
			500					505					510			
Leu	Gln	Ala	Thr	Gln	Glu	Ile	Tyr	Asp	Ser	Leu	His	Lys	Leu	Leu	Ile	
		515					520					525				
Arg	Ser	Thr	Asn	Leu	Lys	Lys	Phe	Lys	Leu	Ser	Tyr	Lys	Tyr	Glu	Met	
	530					535					540					
Glu	Lys	Ser	Lys	Met	Asp	Thr	Phe	Ile	Asp	Leu	Lys	Asn	Ile	Tyr	Glu	
545					550					555					560	
Thr	Leu	Asn	Asn	Leu	Lys	Arg	Cys	Ser	Val	Asn	Ile	Ser	Asn	Pro	His	
				565					570					575		
Gly	Asn	Ile	Ser	Tyr	Glu	Leu	Thr	Asn	Lys	Asp	Ser	Thr	Phe	Tyr	Lys	
			580					585					590			
Phe	Lys	Leu	Thr	Leu	Asn	Gln	Glu	Leu	Gln	His	Ala	Lys	Tyr	Thr	Phe	
		595					600					605				
Lys	Gln	Asn	Glu	Phe	Gln	Phe	Asn	Asn	Val	Lys	Ser	Ala	Lys	Ile	Glu	
	610					615					620					
Ser	Ser	Ser	Leu	Glu	Ser	Leu	Glu	Asp	Ile	Asp	Ser	Leu	Cys	Lys	Ser	
625					630					635				640		
Ile	Ala	Ser	Cys	Lys	Asn	Leu	Gln	Asn	Val	Asn	Ile	Ile	Ala	Ser	Leu	
			645						650				655			
Leu	Tyr	Pro	Asn	Asn	Ile	Gln	Lys	Asn	Pro	Phe	Asn	Lys	Pro	Asn	Leu	
			660					665					670			
Leu	Phe	Phe	Lys	Gln	Phe	Glu	Gln	Leu	Lys	Asn	Leu	Glu	Asn	Val	Ser	
		675					680					685				
Ile	Asn	Cys	Ile	Leu	Asp	Gln	His	Ile	Leu	Asn	Ser	Ile	Ser	Glu	Phe	
	690					695					700					
Leu	Glu	Lys	Asn	Lys	Lys	Ile	Lys	Ala	Phe	Ile	Leu	Lys	Arg	Tyr	Tyr	
705					710					715					720	

Leu Leu Gln Tyr Tyr Leu Asp Tyr Thr Lys Leu Phe Lys Thr Leu Gln  
725 730 735

Gln Leu Pro Glu Leu Asn Gln Val Tyr Ile Asn Gln Gln Leu Glu Glu  
740 745 750

Leu Thr Val Ser Glu Val His Lys Gln Val Trp Glu Asn His Lys Gln  
755 760 765

Lys Ala Phe Tyr Glu Pro Leu Cys Glu Phe Ile Lys Glu Ser Ser Gln  
770 775 780

Thr Leu Gln Leu Ile Asp Phe Asp Gln Asn Thr Val Ser Asp Asp Ser  
785 790 795 800

Ile Lys Lys Ile Leu Glu Ser Ile Ser Glu Ser Lys Tyr His His Tyr  
805 810 815

Leu Arg Leu Asn Pro Ser Gln Ser Ser Ser Leu Ile Lys Ser Glu Asn  
820 825 830

Glu Glu Ile Gln Glu Leu Leu Lys Ala Cys Asp Glu Lys Gly Val Leu  
835 840 845

Val Lys Ala Tyr Tyr Lys Phe Pro Leu Cys Leu Pro Thr Gly Thr Tyr  
850 855 860

Tyr Asp Tyr Asn Ser Asp Arg Trp  
865 870

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu  
1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn  
20 25 30

Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg  
35 40 45

Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val  
50 55 60

Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn  
65 70 75 80

Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn  
85 90 95

Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly  
100 105 110

Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val  
115 120 125

Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe  
130 135 140

Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys  
145 150 155 160

Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys  
165 170 175

Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn  
180 185 190

Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser  
195 200 205

Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr  
210 215 220

Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr  
225 230 235 240

Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile  
245 250 255

Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser  
260 265 270

His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile  
275 280 285

Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys  
290 295 300

Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Leu Ser Leu Pro  
305 310 315 320

Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu  
325 330 335

Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His  
340 345 350

Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu  
355 360 365

Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr  
370 375 380

Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp  
385 390 395 400

Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu  
405 410 415

Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn  
420 425 430

Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu  
435 440 445

Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe  
 450 455 460  
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys  
 465 470 475 480  
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile  
 485 490 495  
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg  
 500 505 510  
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys  
 515 520 525  
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met  
 530 535 540  
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg  
 545 550 555 560  
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn  
 565 570 575  
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp  
 580 585 590  
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val  
 595 600 605  
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr  
 610 615 620  
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile  
 625 630 635 640  
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys  
 645 650 655  
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe  
 660 665 670  
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu  
 675 680 685  
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys  
 690 695 700  
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Asp Thr Val Ile Gln Phe  
 705 710 715 720  
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser  
 725 730 735  
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile  
 740 745 750  
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr  
 755 760 765  
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp  
 770 775 780

His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp  
 785 790 795 800  
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln  
 805 810 815  
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp  
 820 825 830  
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu  
 835 840 845  
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu  
 850 855 860  
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile  
 865 870 875 880  
 His Ile Val Asn

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

DGTDATNARN ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:



Leu Cys Val Ser Tyr Ile Leu Ser Ser Phe Tyr Tyr Ala Asn Leu Glu  
 1 5 10 15  
 Glu Asn Ala Leu Gln Phe Leu Arg Lys Glu Ser Met Asp Pro Glu Lys  
 20 25 30  
 Pro Glu Thr Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Leu Cys Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu  
 1 5 10 15  
 Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu Ser Met Asn Pro Glu Asn  
 20 25 30  
 Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "RNA"

(ix) FEATURE:

- (A) NAME/KEY: modified\_base  
 (B) LOCATION: 12..25  
 (D) OTHER INFORMATION: /mod\_base= OTHER

/note= "The residues located at these positions are  
 2-O-methylribonucleoti..."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TAGACCTGTT AGGUUUUGGG GUUUUG

26

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGGGTTTTTGG GGT

16

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: /note= "expressed sequence tag (EST)  
AA281296"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCAAGTTCC TGC	ACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CAC TTGAAGA	GGGTGCAGCT	GCGGGACGTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGAGGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCG				389

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Ser	Glu	Ile	Glu	Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys
1				5					10					15	
Met	Cys	Leu	Ser	Asp	Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe
			20					25					30		

Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu Gln Ser Phe  
35 40 45  
Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr Val Tyr Phe  
50 55 60  
Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile Thr Ser Met  
65 70 75 80  
Lys Met Glu Ala Phe Glu Lys Ile Asn Glu Asn Asn Val Arg Met Asp  
85 90 95  
Thr Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys  
100 105 110  
Lys Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile  
115 120 125  
Lys Met Gly Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu  
130 135 140  
Arg Pro Val Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser  
145 150 155 160  
Gly Ile Pro Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys  
165 170 175  
Lys Asp Leu Leu Lys His Arg Met Phe Gly Arg Lys Lys Tyr Phe Val  
180 185 190  
Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met  
195 200 205  
Phe Arg Ile Val Lys Lys Lys Leu Lys Asp Pro Glu Phe Val Ile Arg  
210 215 220  
Lys Tyr Ala Thr Ile His Ala Thr Ser  
225 230

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Leu Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys  
1 5 10 15

His Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp  
                   20                                  25                                  30  
 Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys  
                   35                                  40                                  45  
 Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr  
                   50                                  55                                  60  
 Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr  
                   65                                  70                                  75                                  80  
 Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser  
                                   85                                  90                                  95  
 Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn  
                                   100                                  105                                  110  
 Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu  
                   115                                  120                                  125  
 Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln  
                   130                                  135                                  140  
 Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys  
                   145                                  150                                  155                                  160  
 Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln  
                                   165                                  170                                  175  
 Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met  
                                   180                                  185                                  190  
 Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys  
                   195                                  200                                  205  
 Met Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val  
                   210                                  215                                  220  
 Arg Ser Gln Tyr Phe Phe Asn Thr Asn  
                   225                                  230

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /note= "TRT motifs from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Arg Glu Ile Ser Trp Met Gln Val Glu Thr Ser Ala Lys His Phe  
 1 5 10 15  
 Tyr Tyr Phe Asp His Glu Asn Ile Tyr Val Leu Trp Lys Leu Leu Arg  
 20 25 30  
 Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr  
 35 40 45  
 Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys  
 50 55 60  
 Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp Leu Lys Lys  
 65 70 75 80  
 Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu Trp Lys Lys  
 85 90 95  
 Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr  
 100 105 110  
 Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val Asn Ser Asp  
 115 120 125  
 Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu Asn Ser His  
 130 135 140  
 Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp Pro Phe Gly  
 145 150 155 160  
 Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr Glu Glu Phe  
 165 170 175  
 Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe Phe Ala Thr  
 180 185 190  
 Met Asp Ile Glu Lys Cys Tyr Asp Ser Val Asn Arg Glu Lys Leu Ser  
 195 200 205  
 Thr Phe Leu Lys Thr Thr Lys Leu Leu Ser Ser Asp Phe Trp Ile Met  
 210 215 220  
 Thr Ala Gln Ile Leu Lys Arg Lys Asn  
 225 230

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2631
- (D) OTHER INFORMATION: /note= "Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATTTATACTC	ATGAAAATCT	TATTCGAGTT	CATTCAAGAC	AAGCTTGACA	TTGATCTACA	60
GACCAACAGT	ACTTACAAAG	AAAATTTAAA	ATGTGGTCAC	TTCAATGGCC	TCGATGAAAT	120
TCTAACTACG	TGTTTCGCAC	TACCAAATTC	AAGAAAAATA	GCATTACCAT	GCCTTCCTGG	180
TGACTTAAGC	CACAAAGCAG	TCATTGATCA	CTGCATCATT	TACCTGTTGA	CGGGCGAATT	240
ATACAACAAC	GTACTAACAT	TTGGCTATAA	AATAGCTAGA	AATGAAGATG	TCAACAATAG	300
TCTTTTTTGC	CATTCTGCAA	ATGTTAACGT	TACGTTACTG	AAAGGCGCTG	CTTGAAAAAT	360
GTTCCACAGT	TTGGTCGGTA	CATACGCATT	CGTTGATTTA	TTGATCAATT	ATACAGTAAT	420
TCAATTTAAT	GGGCAGTTTT	TCACTCAAAT	CGTGGGTAAC	AGATGTAACG	AACCTCATCT	480
GCCGCCCAAA	TGGGTCCAAC	GATCATCCTC	ATCATCCGCA	ACTGCTGCGC	AAATCAAACA	540
ACTTACAGAA	CCAGTGACAA	ATAACAATTT	CTTACACAAG	CTCAATATAA	ATTCCTCTTC	600
TTTTTTTCCT	TATAGCAAGA	TCCTTCCTTC	ATCATCATCT	ATCAAAAAGC	TAAGTACTTT	660
GAGAGAAGCT	ATTTTTCCCA	CAAATTTGGT	TAAATTCCTT	CAGAGACTAA	AGGTACGAAT	720
TAATTTGACG	CTGCAAAAGC	TATTAAAGAG	ACATAAGCGT	TTGAATTACG	TTTCTATTTT	780
GAATAGTATT	TGCCCACCAT	TGGAAGGGAC	CGTATTGGAC	TTGTCGCATT	TGAGTAGGCA	840
ATCACCAAAG	GAACGAGTCT	TGAAATTTAT	CATTGTTATT	TTACAGAAGT	TATTACCCCA	900
AGAAATGTTT	GGCTCAAAGA	AAAATAAAGG	AAAAATTATC	AAGAATCTAA	ATCTTTTATT	960
AAGTTTACCC	TTAAATGGCT	ATTTACCATT	TGATAGTTTG	TTGAAAAAGT	TAAGATTAAA	1020
GGATTTTCGG	TGGTTGTTCA	TTTCTGATAT	TTGGTTCACC	AAGCACAATT	TTGAAAACTT	1080
GAATCAATTG	GCGATTTGTT	TCATTTCTCT	GCTATTTAGA	CAACTAATTC	CCAAAATTAT	1140
ACAGACTTTT	TTTTACTGCA	CCGAAATATC	TTCTACAGTG	ACAATTGTTT	ACTTTAGACA	1200
TGATACTTGG	AATAAACTTA	TCACCCCTTT	TATCGTAGAA	TATTTTAAGA	CGTACTTAGT	1260
CGAAAACAAC	GTATGTAGAA	ACCATAATAG	TTACACGTTG	TCCAATTTCA	ATCATAGCAA	1320
AATGAGGATT	ATACCAAAAA	AAAGTAATAA	TGAGTTCAGG	ATTATTGCCA	TCCCATGCAG	1380
AGGGGCAGAC	GAAGAAGAAT	TCACAATTTA	TAAGGAGAAT	CACAAAAATG	CTATCCAGCC	1440
CACTCAAAAA	ATTTTAGAAT	ACCTAAGAAA	CAAAAGGCCG	ACTAGTTTTA	CTAAAATATA	1500
TTCTCCAACG	CAAATAGCTG	ACCGTATCAA	AGAATTTAAG	CAGAGACTTT	TAAAGAAATT	1560
TAATAATGTC	TTACCAGAGC	TTTATTTTCAT	GAAATTTGAT	GTCAAATCTT	GCTATGATTC	1620
CATACCAAGG	ATGGAATGTA	TGAGGATACT	CAAGGATGCG	CTAAAAAATG	AAAATGGGTT	1680
TTTCGTTAGA	TCTCAATATT	TCTTCAATAC	CAATACAGGT	GTATTGAAGT	TATTTAATGT	1740
TGTTAACGCT	AGCAGAGTAC	CAAAACCTTA	TGAGCTATAC	ATAGATAATG	TGAGGACGGT	1800

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TEATTTATCA AATCAGGATG TTATAAACGT TGTAGAGATG GAAATATTTA AAACAGCTTT 1860
GTGGGTTGAA GATAAGTGCT ACATTAGAGA AGATGGTCTT TTTCAGGGCT CTAGTTTATC 1920
TGCTCCGATC GTTGATTTGG TGTATGACGA TCTTCTGGAG TTTTATAGCG AGTTTAAAGC 1980
CAGTCCTAGC CAGGACACAT TAATTTTAAA ACTGGCTGAC GATTTTCCTTA TAATATCAAC 2040
AGACCAACAG CAAGTGATCA ATATCAAAAA GCTTGCCATG GGCGGATTTT AAAAATATAA 2100
TGCGAAAGCC AATAGAGACA AAATTTTAGC CGTAAGCTCC CAATCAGATG ATGATACGGT 2160
TATTCAATTT TGTGCAATGC ACATATTTGT TAAAGAATTG GAAGTTTGGA AACATTCAAG 2220
CACAATGAAT AATTTCCATA TCCGTTTCGAA ATCTAGTAAA GGGATATTTT GAAGTTTAAAT 2280
AGCGCTGTTT AACACTAGAA TCTCTTATAA AACCAATTGAC ACAAATTTAA ATTCAACAAA 2340
CACCGTTCTC ATGCAAATTG ATCATGTTGT AAAGAACATT TCGGAATGTT ATAAATCTGC 2400
TTTTAAGGAT CTATCAATTA ATGTTACGCA AAATATGCAA TTTCATTCGT TCTTACAACG 2460
CATCATTGAA ATGACAGTCA GCGGTTGTCC AATTACGAAA TGTGATCCTT TAATCGAGTA 2520
TGAGGTACGA TTCACCATAT TGAATGGATT TTTGGAAAGC CTATCTTCAA ACACATCAAA 2580
ATTTAAAGAT AATATCATTC TTTTGAGAAA GGAAATTCAA CACTTGCAAG C 2631

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(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: /note= "TRT motifs from human"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

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Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu
1           5           10           15
Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu
20           25           30
Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile
35           40           45
Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu
50           55           60
Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu
65           70           75           80

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Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp  
85 90 95  
Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg  
100 105 110  
Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg  
115 120 125  
Ala

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5544 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: join(959..1216, 1273..1353, 1425..1543,  
1595..1857, 1894..2286, 2326..2396, 2436..2705,  
2746..2862, 2914..3083, 3125..3309, 3356..3504,  
3546..3759, 3797..4046, 4086..4252, 4296..4392,  
4435..4597)  
(D) OTHER INFORMATION: /note= "Schizosaccharomyces pombe  
telomerase catalytic subunit (TRT) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGTACCGATT TACTTTCCTT TCTTCATAAG CTAATTGCTT CCTCGAACGC TCCTAAATCT	60
CTGGAAATAT TTTTACAAGA ACTCAATAAC AATACCAAGT CAAATTCCAA TATGAAGGTG	120
TTATTAGTGA TCGATAATAT TTCTATTTTA TCGGTCGTTA CCAAGTATAA GGACAAAAAG	180
AACAACCTTC TTCCCCCTAA AGACTTTTAC TTTATTAATT TACTTTTCAA ATATATTTCTG	240
GGTTCGCTTA CTTTTAATCG TGGTACTGTT TTAGCTGCTA CTTCTAGCCA ACCGCGTGTT	300
TCTACCCCGT CATTGGATAT AGCTCTTGGA GTAGCTCACA GAAATCCTTA CAAATCTTCT	360
GATGAGACTA TATTAGATTC ATTACAGTCC GTGCATATTC TTAACATGGA GCCTTACACT	420
TTAGATGAGT CACGTCGCAT GATGGAGTAT TTGGTATCAT CCAACGTTTG CTTTGAAAAG	480
GTTGATAATT ATTTGCAAAA TCATGTCCTT AGTGGTGGTA ATCCGCGAAA GTTTTTTGAT	540
GCTTGACACAC GTCTAGCATG ATTGAGATAT TCAAAAATTT CTATCCACTA CAACTCCTTT	600
AACGCGGTTT TATTTTCTA TTTTCTATTC TCATGTTGTT CCAAATATGT ATCATCTCGT	660
ATTAGGCTTT TTTCCGTTTT ACTCCTGGAA TCGTACCTTT TTCACTATTC CCCCTAATGA	720
ATAATCTAAA TTAGTTTCGC TTATAATTGA TAGTAGTAGA AAGATTGGTG ATTCTACTCG	780



TGTAATGTTA TTAGTTTAAA GATACTTTGC AAAACATTTA TTAGCTATCA TTATATAAAA	840
AAAATCCTAT AATTATAAAT ATTAATCAAT ATTTGCGGTC ACTATTTATT TAAAACGTTA	900
TGATCAGTAG GACACTTTGC ATATATATAG TTATGCTTAA TGGTTACTTG TAACTTGC	958
ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu 1 5 10 15	1006
AAT CAA TAT GTA TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val 20 25 30	1054
TTG AGA GGG TCG CCG GCA AGC TCG TAT AGC AAT ATA TGC GAA CGC TTG Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu 35 40 45	1102
AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT CAT TCG ACT GTA Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val 50 55 60	1150
GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro 65 70 75 80	1198
AAA TGC TCA CAG TCA GAG GTATATATAT TTTTGTTTG ATTTTTTTCT Lys Cys Ser Gln Ser Glu 85	1246
ATTCGGGATA GCTAATATAT GGGCAG CTA ATA GCG AAT GTT GTA AAA CAG ATG Leu Ile Ala Asn Val Val Lys Gln Met 90 95	1299
TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA CTG ATG AAA GGG TTT Phe Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe 100 105 110	1347
TCC ATG GTAAGGTATT CTAATTGTGA AATATTTACC TGCAATTACT GTTTCAAAGA Ser Met	1403
GATTGTATTT AACCGATAAA G AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA Asn His Glu Asp Phe Arg Ala Met His Val 115 120	1454
AAC GGA GTA CAA AAT GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA Asn Gly Val Gln Asn Asp Leu Val Ser Thr Phe Pro Asn Tyr Leu Ile 125 130 135	1502
TCT ATA CTT GAG TCA AAA AAT TGG CAA CTT TTG TTA GAA AT Ser Ile Leu Glu Ser Lys Asn Trp Gln Leu Leu Leu Glu Ile 140 145 150	1543
GTAAATACCG GTTAAGATGT TGCACACTTT GAACAAGACT GACAAGTATA G T ATC Ile	1598
GGC AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG Gly Ser Asp Ala Met His Tyr Leu Leu Ser Lys Gly Ser Ile Phe Glu 155 160 165 170	1646

GCT CTT CCA AAT GAC AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT Ala Leu Pro Asn Asp Asn Tyr Leu Gln Ile Ser Gly Ile Pro Leu Phe 175 180 185	1694
AAA AAT AAT GTG TTT GAG GAA ACT GTG TCA AAA AAA AGA AAG CGA ACC Lys Asn Asn Val Phe Glu Glu Thr Val Ser Lys Lys Arg Lys Arg Thr 190 195 200	1742
ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA GAA GTT TCC Ile Glu Thr Ser Ile Thr Gln Asn Lys Ser Ala Arg Lys Glu Val Ser 205 210 215	1790
TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC Trp Asn Ser Ile Ser Ile Ser Arg Phe Ser Ile Phe Tyr Arg Ser Ser 220 225 230	1838
TAT AAG AAG TTT AAG CAA G GTA ACTAATA CTGTTATCCT TCATAACTAA Tyr Lys Lys Phe Lys Gln 235 240	1887
TTTTAG AT CTA TAT TTT AAC TTA CAC TCT ATT TGT GAT CGG AAC ACA Asp Leu Tyr Phe Asn Leu His Ser Ile Cys Asp Arg Asn Thr 245 250	1934
GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG CAA TTT GGA CTT ATA Val His Met Trp Leu Gln Trp Ile Phe Pro Arg Gln Phe Gly Leu Ile 255 260 265 270	1982
AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA TCA Asn Ala Phe Gln Val Lys Gln Leu His Lys Val Ile Pro Leu Val Ser 275 280 285	2030
CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT Gln Ser Thr Val Val Pro Lys Arg Leu Leu Lys Val Tyr Pro Leu Ile 290 295 300	2078
GAA CAA ACA GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC Glu Gln Thr Ala Lys Arg Leu His Arg Ile Ser Leu Ser Lys Val Tyr 305 310 315	2126
AAC CAT TAT TGC CCA TAT ATT GAC ACC CAC GAT GAT GAA AAA ATC CTT Asn His Tyr Cys Pro Tyr Ile Asp Thr His Asp Asp Glu Lys Ile Leu 320 325 330	2174
AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG TTT CTT CGA TCC ATT Ser Tyr Ser Leu Lys Pro Asn Gln Val Phe Ala Phe Leu Arg Ser Ile 335 340 345 350	2222
CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA TTT Leu Val Arg Val Phe Pro Lys Leu Ile Trp Gly Asn Gln Arg Ile Phe 355 360 365	2270
GAG ATA ATA TTA AAA G GTATTGTATA AAATTTATTA CCACTAACGA TTTTACCAG AC Glu Ile Ile Leu Lys 370 Asp	2327
CTC GAA ACT TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT Leu Glu Thr Phe Leu Lys Leu Ser Arg Tyr Glu Ser Phe Ser Leu His 375 380 385	2375
TAT TTA ATG AGT AAC ATA AAG GTAATATGCC AAATTTTTTTT ACCATTAATT Tyr Leu Met Ser Asn Ile Lys	2426

390		395	
AACAATCAG ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA AAA AGG TCA	2474		
Ile Ser Glu Ile Glu Trp Leu Val Leu Gly Lys Arg Ser			
400 405			
AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT	2522		
Asn Ala Lys Met Cys Leu Ser Asp Phe Glu Lys Arg Lys Gln Ile Phe			
410 415 420			
GCG GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA	2570		
Ala Glu Phe Ile Tyr Trp Leu Tyr Asn Ser Phe Ile Ile Pro Ile Leu			
425 430 435 440			
CAA TCT TTT TTT TAT ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT	2618		
Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser Asp Leu Arg Asn Arg Thr			
445 450 455			
GTT TAT TTT AGA AAA GAT ATT TGG AAA CTC TTG TGC CGA CCC TTT ATT	2666		
Val Tyr Phe Arg Lys Asp Ile Trp Lys Leu Leu Cys Arg Pro Phe Ile			
460 465 470			
ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG GTATTTTAAA	2715		
Thr Ser Met Lys Met Glu Ala Phe Glu Lys Ile Asn Glu			
475 480 485			
GTATTTTTTG CAAAAGCTA ATATTTTCAG AAC AAT GTT AGG ATG GAT ACT CAG	2769		
Asn Asn Val Arg Met Asp Thr Gln			
490			
AAA ACT ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT	2817		
Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys Asn			
495 500 505			
ACC TTT CGT CTC ATT ACG AAT TTA AGA AAA AGA TTC TTA ATA AAG	2862		
Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu Ile Lys			
510 515 520			
GTATTAATTT TTGGTCATCA ATGTACTTTA CTTCTAATCT ATTATTAGCA G ATG GGT	2919		
Met Gly			
525			
TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967		
Ser Asn Lys Lys Met Leu Val Ser Thr Asn Gln Thr Leu Arg Pro Val			
530 535 540			
GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA	3015		
Ala Ser Ile Leu Lys His Leu Ile Asn Glu Glu Ser Ser Gly Ile Pro			
545 550 555			
TTT AAC TTG GAG GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT	3063		
Phe Asn Leu Glu Val Tyr Met Lys Leu Leu Thr Phe Lys Lys Asp Leu			
560 565 570			
CTT AAG CAC CGA ATG TTT GG GTAATTATAT AATGCGCGAT TCCTCATTAT	3113		
Leu Lys His Arg Met Phe Gly			
575 580			
TAATTTTGCA G G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA AAA TCC	3161		
Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser			
585 590			

TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG Cys Tyr Asp Arg Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys Lys 595 600 605	3209
AAA CTC AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT Lys Leu Lys Asp Pro Glu Phe Val Ile Arg Lys Tyr Ala Thr Ile His 610 615 620 625	3257
GCA ACA AGT GAC CGA GCT ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC Ala Thr Ser Asp Arg Ala Thr Lys Asn Phe Val Ser Glu Ala Phe Ser 630 635 640	3305
TAT T GTAAGTTTAT TTTTTCATTG GAATTTTTTA ACAAATTCTT TTTTAG TT Tyr Phe	3357
GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA Asp Met Val Pro Phe Glu Lys Val Val Gln Leu Leu Ser Met Lys Thr 645 650 655	3405
TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT Ser Asp Thr Leu Phe Val Asp Phe Val Asp Tyr Trp Thr Lys Ser Ser 660 665 670 675	3453
TCT GAA ATT TTT AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT Ser Glu Ile Phe Lys Met Leu Lys Glu His Leu Ser Gly His Ile Val 680 685 690	3501
AAG GTATACCAAT TGTGTAATTG TAATAACACT AATGAACTA G ATA GGA AAT Lys Ile Gly Asn 695	3554
TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA ATT CTG TCA Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser 700 705 710	3602
TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu 715 720 725	3650
TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp 730 735 740	3698
TTC CTC TTT ATA ACA GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT Phe Leu Phe Ile Thr Val Asn Lys Lys Asp Ala Lys Lys Phe Leu Asn 745 750 755	3746
TTA TCT TTA AGA G GTGAGTTGCT GTCATTCCTA AGTTCTAACC GTTGAAG GA Leu Ser Leu Arg Gly	3798
TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA ATA AAC Phe Glu Lys His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn 765 770 775 780	3846
TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC Phe Glu Asn Ser Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser 785 790 795	3894
AAG AAA AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT Lys Lys Arg Met Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu	3942

800	805	810	
GAT ACA TTG TTA GCA TGT CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT Asp Thr Leu Leu Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser 815 820 825			3990
ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG AAA TCT TTT TTT TAC AAA Thr Ser Val Glu Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys 830 835 840			4038
ATT CTA AG GTATACTGTG TAACTGAATA ATAGCTGACA AATAATCAG A TCG Ile Leu Arg Ser 845			4089
AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser 850 855 860			4137
AAA TTC AAT TCT TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys 865 870 875 880			4185
ATG AGA GCA CAA GCA TAC TTA AAA AGG ATG AAG GAT ATA TTT ATT CCC Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro 885 890 895			4233
CAA AGA ATG TTC ATA ACG G GTGAGTACTT ATTTTAACTA GAAAAGTCAT Gln Arg Met Phe Ile Thr 900			4282
TAATTAACCT TAG AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA Asp Leu Leu Asn Val Ile Gly Arg Lys Ile Trp Lys 905 910			4330
AAG TTG GCC GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu Ser Ser 915 920 925 930			4378
GCA GAA GTC AAA TG GTACGTGTCG GTCTCGAGAC TTCAGCAATA TTGACACATC Ala Glu Val Lys Trp 935			4432
AG G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA CCC TCT TTC AAA Leu Phe Cys Leu Gly Met Arg Asp Gly Leu Lys Pro Ser Phe Lys 940 945 950			4480
TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr Gln Phe Gln Ser Leu Thr 955 960 965			4528
GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA Asp Leu Ile Lys Pro Leu Arg Pro Val Leu Arg Gln Val Leu Phe Leu 970 975 980			4576
CAT AGA AGA ATA GCT GAT TAATGTCATT TTCAATTTAT TATATACATC His Arg Arg Ile Ala Asp 985			4624
CTTTATTACT GGTGTCTTAA ACAATATTAT TACTAAGTAT AGCTGACCCC CAAAGCAAGC			4684
ATACTATAGG ATTTCTAGTA AAGTAAAATT AATCTCGTTA TTAGTTTTGA TTGACTTGTC			4744

TTTATCCTTA TACTTTTAAG AAAGATTGAC AGTGGTTGCT GACTACTGCC CACATGCCCCA 4804  
 TTAAACGGGA GTGGTTAAAC ATTAAAAGTA ATACATGAGG CTAATCTCCT TTCATTTAGA 4864  
 ATAAGGAAAG TGGTTTTCTA TAATGAATAA TGCCCGCACT AATGCAAAAA GACGAAGATT 4924  
 ATCTTCTAAA CAAGGGGGAT TAAGCATATC CGAAGGAAAA GAGAGTAATA TACCCAGTGT 4984  
 TGTTGAAGAA AGCAAGGATA ATTTGGAACA AGCTTCTGCA GATGACAGGC TAAATTTTGG 5044  
 TGACCGAATT TTGGTAAAAG CCCCAGGTTA TCCATGGTGG CCGGCCTTGC TACTGAGACG 5104  
 AAAAGAACT AAGGATAGTT TGAATACTAA TAGCTCATTT AATGTCTTAT ATAAGGTTTTT 5164  
 GTTTTTTCCT GACTTCAATT TTGCATGGGT GAAAAGAAAT AGTGTTAAGC CATTATTGGA 5224  
 TTCCGAAATA GCCAAATTTT TTGGTTCCTC AAAGCGGAAG TCTAAAGAAC TTATTGAAGC 5284  
 TTATGAGGCT TCAAAAACCT CTCCTGATTT AAAGGAGGAA TCTTCCACCG ATGAGGAAAT 5344  
 GGATAGCTTA TCAGCTGCTG AGGAGAAGCC TAATTTTTTG CAAAAAGAA AATATCATTG 5404  
 GGAGACATCT CTTGATGAAT CAGATGCGGA GAGTATCTCC AGCGGATCCT TGATGTCAAT 5464  
 AACTTCTATT TCTGAAATGT ATGGTCCTAC TGTCGCTTCG ACTTCTCGTA GCTCTACGCA 5524  
 GTTAAGTGAC CAAAGGTACC 5544

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Glu His His Thr Pro Lys Ser Arg Ile Leu Arg Phe Leu Glu  
 1 5 10 15  
 Asn Gln Tyr Val Tyr Leu Cys Thr Leu Asn Asp Tyr Val Gln Leu Val  
 20 25 30  
 Leu Arg Gly Ser Pro Ala Ser Ser Tyr Ser Asn Ile Cys Glu Arg Leu  
 35 40 45  
 Arg Ser Asp Val Gln Thr Ser Phe Ser Ile Phe Leu His Ser Thr Val  
 50 55 60  
 Val Gly Phe Asp Ser Lys Pro Asp Glu Gly Val Gln Phe Ser Ser Pro  
 65 70 75 80  
 Lys Cys Ser Gln Ser Glu Leu Ile Ala Asn Val Val Lys Gln Met Phe  
 85 90 95  
 Asp Glu Ser Phe Glu Arg Arg Arg Asn Leu Leu Met Lys Gly Phe Ser  
 100 105 110  
 Met Asn His Glu Asp Phe Arg Ala Met His Val Asn Gly Val Gln Asn

115					120					125					
Asp	Leu	Val	Ser	Thr	Phe	Pro	Asn	Tyr	Leu	Ile	Ser	Ile	Leu	Glu	Ser
130						135					140				
Lys	Asn	Trp	Gln	Leu	Leu	Leu	Glu	Ile	Ile	Gly	Ser	Asp	Ala	Met	His
145				150						155					160
Tyr	Leu	Leu	Ser	Lys	Gly	Ser	Ile	Phe	Glu	Ala	Leu	Pro	Asn	Asp	Asn
				165					170					175	
Tyr	Leu	Gln	Ile	Ser	Gly	Ile	Pro	Leu	Phe	Lys	Asn	Asn	Val	Phe	Glu
			180					185					190		
Glu	Thr	Val	Ser	Lys	Lys	Arg	Lys	Arg	Thr	Ile	Glu	Thr	Ser	Ile	Thr
		195					200					205			
Gln	Asn	Lys	Ser	Ala	Arg	Lys	Glu	Val	Ser	Trp	Asn	Ser	Ile	Ser	Ile
	210					215					220				
Ser	Arg	Phe	Ser	Ile	Phe	Tyr	Arg	Ser	Ser	Tyr	Lys	Lys	Phe	Lys	Gln
225						230					235				240
Asp	Leu	Tyr	Phe	Asn	Leu	His	Ser	Ile	Cys	Asp	Arg	Asn	Thr	Val	His
				245					250					255	
Met	Trp	Leu	Gln	Trp	Ile	Phe	Pro	Arg	Gln	Phe	Gly	Leu	Ile	Asn	Ala
			260					265						270	
Phe	Gln	Val	Lys	Gln	Leu	His	Lys	Val	Ile	Pro	Leu	Val	Ser	Gln	Ser
			275				280					285			
Thr	Val	Val	Pro	Lys	Arg	Leu	Leu	Lys	Val	Tyr	Pro	Leu	Ile	Glu	Gln
			290			295					300				
Thr	Ala	Lys	Arg	Leu	His	Arg	Ile	Ser	Leu	Ser	Lys	Val	Tyr	Asn	His
305						310					315				320
Tyr	Cys	Pro	Tyr	Ile	Asp	Thr	His	Asp	Asp	Glu	Lys	Ile	Leu	Ser	Tyr
				325					330					335	
Ser	Leu	Lys	Pro	Asn	Gln	Val	Phe	Ala	Phe	Leu	Arg	Ser	Ile	Leu	Val
			340					345					350		
Arg	Val	Phe	Pro	Lys	Leu	Ile	Trp	Gly	Asn	Gln	Arg	Ile	Phe	Glu	Ile
			355				360					365			
Ile	Leu	Lys	Asp	Leu	Glu	Thr	Phe	Leu	Lys	Leu	Ser	Arg	Tyr	Glu	Ser
			370			375					380				
Phe	Ser	Leu	His	Tyr	Leu	Met	Ser	Asn	Ile	Lys	Ile	Ser	Glu	Ile	Glu
385						390					395				400
Trp	Leu	Val	Leu	Gly	Lys	Arg	Ser	Asn	Ala	Lys	Met	Cys	Leu	Ser	Asp
				405					410					415	
Phe	Glu	Lys	Arg	Lys	Gln	Ile	Phe	Ala	Glu	Phe	Ile	Tyr	Trp	Leu	Tyr
			420					425					430		
Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr	Ile	Thr	Glu
			435				440					445			

Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys	Asp	Ile	Trp	450	455	460
Lys	Leu	Leu	Cys	Arg	Pro	Phe	Ile	Thr	Ser	Met	Lys	Met	Glu	Ala	Phe	465	470	475
Glu	Lys	Ile	Asn	Glu	Asn	Asn	Val	Arg	Met	Asp	Thr	Gln	Lys	Thr	Thr	485	490	495
Leu	Pro	Pro	Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	500	505	510
Leu	Ile	Thr	Asn	Leu	Arg	Lys	Arg	Phe	Leu	Ile	Lys	Met	Gly	Ser	Asn	515	520	525
Lys	Lys	Met	Leu	Val	Ser	Thr	Asn	Gln	Thr	Leu	Arg	Pro	Val	Ala	Ser	530	535	540
Ile	Leu	Lys	His	Leu	Ile	Asn	Glu	Glu	Ser	Ser	Gly	Ile	Pro	Phe	Asn	545	550	555
Leu	Glu	Val	Tyr	Met	Lys	Leu	Leu	Thr	Phe	Lys	Lys	Asp	Leu	Leu	Lys	565	570	575
His	Arg	Met	Phe	Gly	Arg	Lys	Lys	Tyr	Phe	Val	Arg	Ile	Asp	Ile	Lys	580	585	590
Ser	Cys	Tyr	Asp	Arg	Ile	Lys	Gln	Asp	Leu	Met	Phe	Arg	Ile	Val	Lys	595	600	605
Lys	Lys	Leu	Lys	Asp	Pro	Glu	Phe	Val	Ile	Arg	Lys	Tyr	Ala	Thr	Ile	610	615	620
His	Ala	Thr	Ser	Asp	Arg	Ala	Thr	Lys	Asn	Phe	Val	Ser	Glu	Ala	Phe	625	630	635
Ser	Tyr	Phe	Asp	Met	Val	Pro	Phe	Glu	Lys	Val	Val	Gln	Leu	Leu	Ser	645	650	655
Met	Lys	Thr	Ser	Asp	Thr	Leu	Phe	Val	Asp	Phe	Val	Asp	Tyr	Trp	Thr	660	665	670
Lys	Ser	Ser	Ser	Glu	Ile	Phe	Lys	Met	Leu	Lys	Glu	His	Leu	Ser	Gly	675	680	685
His	Ile	Val	Lys	Ile	Gly	Asn	Ser	Gln	Tyr	Leu	Gln	Lys	Val	Gly	Ile	690	695	700
Pro	Gln	Gly	Ser	Ile	Leu	Ser	Ser	Phe	Leu	Cys	His	Phe	Tyr	Met	Glu	705	710	715
Asp	Leu	Ile	Asp	Glu	Tyr	Leu	Ser	Phe	Thr	Lys	Lys	Lys	Gly	Ser	Val	725	730	735
Leu	Leu	Arg	Val	Val	Asp	Asp	Phe	Leu	Phe	Ile	Thr	Val	Asn	Lys	Lys	740	745	750
Asp	Ala	Lys	Lys	Phe	Leu	Asn	Leu	Ser	Leu	Arg	Gly	Phe	Glu	Lys	His	755	760	765
Asn	Phe	Ser	Thr	Ser	Leu	Glu	Lys	Thr	Val	Ile	Asn	Phe	Glu	Asn	Ser	770	775	780



Asn Gly Ile Ile Asn Asn Thr Phe Phe Asn Glu Ser Lys Lys Arg Met  
 785 790 795 800  
 Pro Phe Phe Gly Phe Ser Val Asn Met Arg Ser Leu Asp Thr Leu Leu  
 805 810 815  
 Ala Cys Pro Lys Ile Asp Glu Ala Leu Phe Asn Ser Thr Ser Val Glu  
 820 825 830  
 Leu Thr Lys His Met Gly Lys Ser Phe Phe Tyr Lys Ile Leu Arg Ser  
 835 840 845  
 Ser Leu Ala Ser Phe Ala Gln Val Phe Ile Asp Ile Thr His Asn Ser  
 850 855 860  
 Lys Phe Asn Ser Cys Cys Asn Ile Tyr Arg Leu Gly Tyr Ser Met Cys  
 865 870 875 880  
 Met Arg Ala Gln Ala Tyr Leu Lys Arg Met Lys Asp Ile Phe Ile Pro  
 885 890 895  
 Gln Arg Met Phe Ile Thr Asp Leu Leu Asn Val Ile Gly Arg Lys Ile  
 900 905 910  
 Trp Lys Lys Leu Ala Glu Ile Leu Gly Tyr Thr Ser Arg Arg Phe Leu  
 915 920 925  
 Ser Ser Ala Glu Val Lys Trp Leu Phe Cys Leu Gly Met Arg Asp Gly  
 930 935 940  
 Leu Lys Pro Ser Phe Lys Tyr His Pro Cys Phe Glu Gln Leu Ile Tyr  
 945 950 955 960  
 Gln Phe Gln Ser Leu Thr Asp Leu Ile Lys Pro Leu Arg Pro Val Leu  
 965 970 975  
 Arg Gln Val Leu Phe Leu His Arg Arg Ile Ala Asp  
 980 985

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = guanosine modified by a biotin group"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

NCCTATTTYT TYTAYNNNAC NGA

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Phe Phe Tyr Xaa Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCAGATATNA DNARRAARTC RTC

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Phe, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asp Asp Phe Leu Xaa Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACAATGMGNH TNHTNCCNAA RAA

23

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..3
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = Leu or Ile"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Arg Xaa Xaa Pro Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ACGAATCKNG GDATNSWRTC RTARCA

26

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Cys Tyr Asp Ser Ile Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAATTCTCRT ARCANSWYTT DATRTC

26

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asp Ile Lys Ser Cys Tyr Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GATTACTCCC GAAGAAAGGA TCTTTCCGTC CAATCATGAC TTTCTTAAGA AAGGACAAGC	60
AAAAAATAT TAAGTTAAAT CTAAATTAAA TTCTAATGGA TAGCCAACTT GTGTTTAGGA	120
ATTTAAAAGA CATGCTGGGA TAAAGATAG GATACTCAGT CTTTGATAAT AAACAAATTT	180
CAGAAAAATT TGCCTAATTC ATAGAGAAAT GGAAAAATAA AGGAAGACCT CAGCTATATT	240
ATGTCACTCT AGACATAAAG ACTTGCTAC	269

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 474 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAACACAAGG AAGGAAGTCA AATATTCTAT TACCGTAAAC CAATATGGAA ATTAGTGAGT	60
AAATTAACTA TTGTCAAAGT AAGAATTTAG TTTTCTGAAA AGAATAAATA AATGAAAAAT	120
AATTTTTATC AAAAAATTTA GCTTGAAGAG GAGAATTTGG AAAAAGTTGA AGAAAAATTG	180
ATACCAGAAG ATTCATTTTA GAAATACCCT CAAGGAAAGC TAAGGATTAT ACCTAAAAAA	240
GGATCTTTCC GTCCAATCAT GACTTTCTTA AGAAAGGACA AGCAAAAAAA TATTAAGTTA	300
AATCTAAATT AAATTCTAAT GGATAGCCAA CTTGTGTTTA GGAATTTAAA AGACATGCTG	360
GGATAAAAGA TAGGATACTC AGTCTTTGAT AATAAACAAA TTTCAGAAAA ATTTGCCTAA	420
TTCATAGAGA AATGGAAAAA TAAAGGAAGA CCTCAGCTAT ATTATGTCAC TCTA	474

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Lys	His	Lys	Glu	Gly	Ser	Gln	Ile	Phe	Tyr	Tyr	Arg	Lys	Pro	Ile	Trp
1			5						10					15	
Lys	Leu	Val	Ser	Lys	Leu	Thr	Ile	Val	Lys	Val	Arg	Ile	Gln	Phe	Ser
		20						25					30		
Glu	Lys	Asn	Lys	Gln	Met	Lys	Asn	Asn	Phe	Tyr	Gln	Lys	Ile	Gln	Leu
		35					40					45			
Glu	Glu	Glu	Asn	Leu	Glu	Lys	Val	Glu	Glu	Lys	Leu	Ile	Pro	Glu	Asp
	50					55					60				
Ser	Phe	Gln	Lys	Tyr	Pro	Gln	Gly	Lys	Leu	Arg	Ile	Ile	Pro	Lys	Lys
65					70					75				80	
Gly	Ser	Phe	Arg	Pro	Ile	Met	Thr	Phe	Leu	Arg	Lys	Asp	Lys	Gln	Lys
			85						90					95	
Asn	Ile	Lys	Leu	Asn	Leu	Asn	Gln	Ile	Leu	Met	Asp	Ser	Gln	Leu	Val
			100					105					110		
Phe	Arg	Asn	Leu	Lys	Asp	Met	Leu	Gly	Gln	Lys	Ile	Gly	Tyr	Ser	Val
		115					120					125			
Phe	Asp	Asn	Lys	Gln	Ile	Ser	Glu	Lys	Phe	Ala	Gln	Phe	Ile	Glu	Lys

130

135

140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Phe Tyr Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe  
 1 5 10 15  
 Arg His Asp Thr Trp Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr  
 20 25 30  
 Phe Lys Thr Tyr Leu Val Glu Asn Asn Val Cys Arg Asn His Asn Ser  
 35 40 45  
 Tyr Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys  
 50 55 60  
 Lys Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala  
 65 70 75 80  
 Asp Glu Glu Glu Phe Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile  
 85 90 95  
 Gln Pro Thr Gln Lys Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr  
 100 105 110  
 Ser Phe Thr Lys Ile Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys  
 115 120 125  
 Glu Phe Lys Gln Arg Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu  
 130 135 140  
 Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr  
 1 5 10 15  
 Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys Met Ser Ile Ala Asp  
 20 25 30  
 Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu Lys Glu Val Glu Glu  
 35 40 45  
 Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro  
 50 55 60  
 Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val  
 65 70 75 80  
 Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr Thr Asn Thr Lys Leu Leu  
 85 90 95  
 Asn Ser His Leu Met Leu Lys Thr Leu Lys Asn Arg Met Phe Lys Asp  
 100 105 110  
 Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp Asp Val Met Lys Lys Tyr  
 115 120 125  
 Glu Glu Phe Val Cys Lys Trp Lys Gln Val Gly Gln Pro Lys Leu Phe  
 130 135 140  
 Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys His Lys Glu Gly Ser Gln Ile Phe Tyr Tyr Arg Lys Pro Ile Trp  
 1 5 10 15  
 Lys Leu Val Ser Lys Leu Thr Ile Val Lys Val Arg Ile Gln Phe Ser  
 20 25 30  
 Glu Lys Asn Lys Gln Met Lys Asn Asn Phe Tyr Gln Lys Ile Gln Leu  
 35 40 45  
 Glu Glu Glu Asn Leu Glu Lys Val Glu Glu Lys Leu Ile Pro Glu Asp  
 50 55 60  
 Ser Phe Gln Lys Tyr Pro Gln Gly Lys Leu Arg Ile Ile Pro Lys Lys  
 65 70 75 80  
 Gly Ser Phe Arg Pro Ile Met Thr Phe Leu Arg Lys Asp Lys Gln Lys  
 85 90 95

Asn Ile Lys Leu Asn Leu Asn Gln Ile Leu Met Asp Ser Gln Leu Val  
100 105 110

Phe Arg Asn Leu Lys Asp Met Leu Gly Gln Lys Ile Gly Tyr Ser Val  
115 120 125

Phe Asp Asn Lys Gln Ile Ser Glu Lys Phe Ala Gln Phe Ile Glu Lys  
130 135 140

Trp Lys Asn Lys Gly Arg Pro Gln Leu Tyr Tyr Val Thr Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1007 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser Ala  
1 5 10 15

Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser Trp  
20 25 30

Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr Lys  
35 40 45

Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala Thr  
50 55 60

Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys Glu  
65 70 75 80

Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu Val  
85 90 95

Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln Cys  
100 105 110

Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu Leu  
115 120 125

Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp Asn  
130 135 140

Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr Thr  
145 150 155 160

Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln Phe  
165 170 175

Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe Asp  
180 185 190



Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys Cys  
 195 200 205  
 Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu Asn  
 210 215 220  
 Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg Ile  
 225 230 235 240  
 Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys His  
 245 250 255  
 Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala Gln  
 260 265 270  
 Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys Leu  
 275 280 285  
 Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val Lys  
 290 295 300  
 Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro Glu  
 305 310 315 320  
 Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys Thr  
 325 330 335  
 Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr Thr  
 340 345 350  
 Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn Ile  
 355 360 365  
 Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln Lys  
 370 375 380  
 Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His Lys  
 385 390 395 400  
 Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met Gln  
 405 410 415  
 Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn Ile  
 420 425 430  
 Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val Val  
 435 440 445  
 Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser Tyr  
 450 455 460  
 Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met Lys  
 465 470 475 480  
 Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln Glu  
 485 490 495  
 Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly Lys  
 500 505 510  
 Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr Phe  
 515 520 525

Asn	Lys	Lys	Ile	Val	Asn	Ser	Asp	Arg	Lys	Thr	Thr	Lys	Leu	Thr	Thr	
530						535					540					
Asn	Thr	Lys	Leu	Leu	Asn	Ser	His	Leu	Met	Leu	Lys	Thr	Leu	Lys	Asn	
545					550					555					560	
Arg	Met	Phe	Lys	Asp	Pro	Phe	Gly	Phe	Ala	Val	Phe	Asn	Tyr	Asp	Asp	
				565					570					575		
Val	Met	Lys	Lys	Tyr	Glu	Glu	Phe	Val	Cys	Lys	Trp	Lys	Gln	Val	Gly	
			580					585					590			
Gln	Pro	Lys	Leu	Phe	Phe	Ala	Thr	Met	Asp	Ile	Glu	Lys	Cys	Tyr	Asp	
		595					600					605				
Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys	Leu	
	610					615						620				
Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg	Lys	
625					630					635					640	
Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met	Lys	
				645					650					655		
Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly	Gln	
			660				665						670			
Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu	Asn	
		675					680					685				
Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe	Lys	
	690					695					700					
Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn	Tyr	
705					710					715					720	
Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro	Gln	
				725					730					735		
Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr	Leu	
			740					745					750			
Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro	Glu	
		755					760					765				
Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu	Leu	
	770					775					780					
Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu	Ile	
785					790					795					800	
Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu	Gln	
				805					810					815		
Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met	Asp	
			820					825					830			
Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile	Gly	
		835					840					845				
Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn	Leu	
850						855					860					

Arg Ile Glu Gly Ile Leu Cys Thr Leu Asn Leu Asn Met Gln Thr Lys  
865 870 875 880

Lys Ala Ser Met Trp Leu Lys Lys Lys Leu Lys Ser Phe Leu Met Asn  
885 890 895

Asn Ile Thr His Tyr Phe Arg Lys Thr Ile Thr Thr Glu Asp Phe Ala  
900 905 910

Asn Lys Thr Leu Asn Lys Leu Phe Ile Ser Gly Gly Tyr Lys Tyr Met  
915 920 925

Gln Cys Ala Lys Glu Tyr Lys Asp His Phe Lys Lys Asn Leu Ala Met  
930 935 940

Ser Ser Met Ile Asp Leu Glu Val Ser Lys Ile Ile Tyr Ser Val Thr  
945 950 955 960

Arg Ala Phe Phe Lys Tyr Leu Val Cys Asn Ile Lys Asp Thr Ile Phe  
965 970 975

Gly Glu Glu His Tyr Pro Asp Phe Phe Leu Ser Thr Leu Lys His Phe  
980 985 990

Ile Glu Ile Phe Ser Thr Lys Lys Tyr Ile Phe Asn Arg Val Cys  
995 1000 1005

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTGAAGGCAC TGTTACGCG

19

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGATGATT TCTTGTGG

19

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGCTCCTGC GTTTGGTGG

19

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTGGACACTC AGCCCTTGG

19

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCAGGTGTG CTGGACACT

19

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TTTGATGATG CTGGCGATG

19

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGGGCTCGTC TTCTACAGG

19

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGCAGGAGG ATCTTG TAG

19

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGACCCCAGG AGTGGCAGG

19

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TCAAGCTGAC TCGACACCG

19

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGGCGTGACA GGGCTGC

17

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCTGAAGGCT GAGTGTCC

18

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TAGTCCATGT TCACAATCG

19

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 22..1716  
 (D) OTHER INFORMATION: /note= "EcoRI-NotI insert of  
 clone 712562 encoding 63 kDa

## telomerase protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCAAGTTCC	TGCACTGGCT	GATGAGTGTG	TACGTCGTCG	AGCTGCTCAG	GTCTTTCTTT	60
TATGTCACGG	AGACCACGTT	TCAAAAGAAC	AGGCTCTTTT	TCTACCGGAA	GAGTGTCTGG	120
AGCAAGTTGC	AAAGCATTGG	AATCAGACAG	CACTTGAAGA	GGGTGCAGCT	GCGGGAGCTG	180
TCGGAAGCAG	AGGTCAGGCA	GCATCGGGAA	GCCAGGCCCG	CCCTGCTGAC	GTCCAGACTC	240
CGCTTCATCC	CCAAGCCTGA	CGGGCTGCGG	CCGATTGTGA	ACATGGACTA	CGTCGTGGGA	300
GCCAGAACGT	TCCGCAGAGA	AAAGARGGCC	GAGCGTCTCA	CCTCGAGGGT	GAAGGCACTG	360
TTCAGCGTGC	TCAACTACGA	GCGGGCGCGG	CGCCCCGGCC	TCCTGGGCGC	CTCTGTGCTG	420
GGCCTGGACG	ATATCCACAG	GGCCTGGCGC	ACCTTCGTGC	TGCGTGTGCG	GGCCAGGAC	480
CCGCCGCCTG	AGCTGTACTT	TGTCAAGGTG	GATGTGACGG	GCGCGTACGA	CACCATCCCC	540
CAGGACAGGC	TCACGGAGGT	CATCGCCAGC	ATCATCAAAC	CCCAGAACAC	GTACTGCGTG	600
CGTCGGTATG	CCGTGGTCCA	GAAGGCCGCC	ATGGGCACGT	CCGCAAGGCC	TTCAAGAGCC	660
ACGTCTACG	TCCAGTGCCA	GGGGATCCCG	CAGGGCTCCA	TCCTCTCCAC	GCTGCTCTGC	720
AGCCTGTGCT	ACGGCGACAT	GGAGAACAAG	CTGTTTGCGG	GGATTGCGCG	GGACGGGCTG	780
CTCCTGCGTT	TGGTGGATGA	TTTCTTGTTG	GTGACACCTC	ACCTCACCCA	CGCGAAAACC	840
TTCCTCAGGA	CCCTGGTCCG	AGGTGTCCCT	GAGTATGGCT	GCGTGGTGAA	CTTGCGGAAG	900
ACAGTGGTGA	ACTTCCCTGT	AGAAGACGAG	GCCCTGGGTG	GCACGGCTTT	TGTTTCAGATG	960
CCGGCCACG	GCCTATTCCC	CTGGTGCGGC	CTGCTGCTGG	ATACCCGGAC	CCTGGAGGTG	1020
CAGAGCGACT	ACTCCAGCTA	TGCCCCGACC	TCCATCAGAG	CCAGTCTCAC	CTTCAACCGC	1080
GGCTTCAAGG	CTGGGAGGAA	CATGCGTCGC	AAACTCTTTG	GGGTCTTGCG	GCTGAAGTGT	1140
CACAGCCTGT	TTCTGGATTT	GCAGGTGAAC	AGCCTCCAGA	CGGTGTGCAC	CAACATCTAC	1200
AAGATCCTCC	TGCTGCAGGC	GTACAGGTTT	CACGCATGTG	TGCTGCAGCT	CCCATTTTCAT	1260
CAGCAAGTTT	GGAAGAACCC	ACATTTTTTC	TGCGCGTCAT	CTCTGACACG	GCTCCCTCTG	1320
CTACTCCATC	CTGAAAGCCA	AGAACGCAGG	GATGTCGCTG	GGGGCCAAGG	GCGCCGCCGG	1380
CCCTCTGCCC	TCCGAGGCCG	TGCAGTGGCT	GTGCCACCAA	GCATTCTTGC	TCAAGCTGAC	1440
TCGACACCGT	GTCACCTACG	TGCCACTCCT	GGGGTCACTC	AGGACAGCCC	AGACGCAGCT	1500
GAGTCGGAAG	CTCCCGGGGA	CGACGCTGAC	TGCCCTGGAG	GCCGCAGCCA	ACCCGGCACT	1560
GCCCTCAGAC	TTCAAGACCA	TCCTGGACTG	ATGGCCACCC	GCCCACAGCC	AGGCCGAGAG	1620
CAGACACCAG	CAGCCCTGTC	ACGCCGGGCT	TATACGTCCC	AGGGAGGGAG	GGGCGGCCCA	1680
CACCCAGGCC	TGCACCGCTG	GGAGTCTGAG	GCCTGAGTGA	GTGTTTGGCC	GAGGCCTGCA	1740

TGTCCGGCTG AAGGCTGAGT GTCCGGCTGA GGCCTGAGCG AGTGTCCAGC CAAGGGCTGA 1800  
 GTGTCCAGCA CACCTGCGTT TTCACTTCCC CACAGGCTGG CGTTCGGTCC ACCCCAGGGC 1860  
 CAGCTTTTCC TCACCAGGAG CCCGGCTTCC ACTCCCCACA TAGGAATAGT CCATCCCCAG 1920  
 ATTCGCCATT GTTCACCCTT CGCCCTGCCT TCCTTTGCCT TCCACCCCCA CCATTCAGGT 1980  
 GGAGACCCTG AGAAGGACCC TGGGAGCTTT GGAATTGAG AGTGACCAA GGTGTGCCCT 2040  
 GTACACAGGC GAGGACCCTG CACCTGGATG GGGGTCCCTG TGGGTCAAAT TGGGGGGAGG 2100  
 TGCTGTGGGA GTAAAATACT GAATATATGA GTTTTTTCACT TTTGGAAAAA AAAAAAAAAA 2160  
 AAAAAAAAAA A 2171

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "63 kDa telomerase protein encoded by ORF of EcoRI-NotI insert of clone 712562"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	Thr
1				5					10					15	
Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	Val
			20					25					30		
Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	Val
		35					40					45			
Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	Ala
	50					55				60					
Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	Asp
65					70					75				80	
Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	Thr
			85					90					95		
Phe	Arg	Arg	Glu	Lys	Xaa	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	Ala
			100				105						110		
Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	Leu
			115				120					125			



Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	Thr		
130						135					140						
Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	Phe		
145					150					155					160		
Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile	Pro	Gln	Asp	Arg		
				165					170					175			
Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys		
			180					185					190				
Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	Met	Gly	Thr	Ser	Ala		
		195					200					205					
Arg	Pro	Ser	Arg	Ala	Thr	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln		
	210					215					220						
Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met		
225					230					235					240		
Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg		
				245					250						255		
Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys		
			260					265					270				
Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val		
		275					280					285					
Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp	Glu	Ala		
	290					295					300						
Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu	Phe	Pro		
305					310					315					320		
Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln	Ser	Asp		
				325					330					335			
Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala	Ser	Leu	Thr	Phe	Asn		
			340					345					350				
Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg	Lys	Leu	Phe	Gly	Val		
		355					360					365					
Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp	Leu	Gln	Val	Asn	Ser		
	370					375					380						
Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	Ala		
385					390					395					400		
Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	Val		
				405					410					415			
Trp	Lys	Asn	Pro	His	Phe	Ser	Cys	Ala	Ser	Ser	Leu	Thr	Arg	Leu	Pro		
			420					425					430				
Leu	Leu	Leu	His	Pro	Glu	Ser	Gln	Glu	Arg	Arg	Asp	Val	Ala	Gly	Gly		
		435					440					445					
Gln	Gly	Arg	Arg	Arg	Pro	Ser	Ala	Leu	Arg	Gly	Arg	Ala	Val	Ala	Val		
450						455					460						

Pro Pro Ser Ile Pro Ala Gln Ala Asp Ser Thr Pro Cys His Leu Arg  
 465 470 475 480

Ala Thr Pro Gly Val Thr Gln Asp Ser Pro Asp Ala Ala Glu Ser Glu  
 485 490 495

Ala Pro Gly Asp Asp Ala Asp Cys Pro Gly Gly Arg Ser Gln Pro Gly  
 500 505 510

Thr Ala Leu Arg Leu Gln Asp His Pro Gly Leu Met Ala Thr Arg Pro  
 515 520 525

Gln Pro Gly Arg Glu Gln Thr Pro Ala Ala Leu Ser Arg Arg Ala Tyr  
 530 535 540

Thr Ser Gln Gly Gly Arg Gly Gly Pro His Pro Gly Leu His Arg Trp  
 545 550 555 560

Glu Ser Glu Ala

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCAGTGAGCA GAGTGACGAG GACTCGAGCT CAAGCTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CCAGTGAGCA GAGTGACG

18

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAGGACTCGA GCTCAAGC

18

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CACTGATCCT TTCTTTTTCG TAAACGATAG GT

32

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATCAATCAA ATCTTCCATA TAGAAATGAC A

31

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = 5'-phosphorylated guanosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

NGGCCGTGTT GGCCTAGTTC TCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAGGAGGAGA AGAGCAGAGA ACTAGGCCAA CACGCCCC

38

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTGTCATTTC TATATGGAAG ATTTGATTGA TG

32

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ACCTATCGTT TACGAAAAG AAAGGATCAG TG

32

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAGTGACATA ATATACGTGA

20

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe  
 1                      5                      10                      15  
 Tyr Arg Lys Ser Val Trp Ser Lys  
                     20

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser Glu Ala Glu  
 1                      5                      10                      15  
 Val Arg Gln His Arg Glu Ala  
                     20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg  
 1                      5                      10                      15  
 Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu  
                     20                      25

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu  
1 5 10 15

Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln  
20 25

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
1 5 10 15

Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Asp Val Ser  
20 25 30

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro Asp Gly  
1 5 10 15

Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

YARACHAARG GHATYCCHYA RGG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Gln Thr Lys Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

NGTNATDARD ARRTARTCRT C

21

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Asp Asp Tyr Leu Leu Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile Leu Ser Ser Phe  
1 5 10 15  
Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe Leu Arg Asp Glu  
20 25 30  
Ser Met Asn Pro Glu Asn Pro Asn Val Asn Leu Leu Met Arg Leu Thr  
35 40 45  
Asp Asp Tyr Leu Leu Ile Thr  
50 55

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Ile Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu Asp Leu Ile  
1 5 10 15  
Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys Gly Ser Val Leu Leu Arg  
20 25 30  
Val Val

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile Val Asp Leu  
1 5 10 15  
Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys Ala Ser Pro  
20 25 30  
Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
35 40 45  
Ser



(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gln Lys Val Gly Ile Pro Gln Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAAAAAGTTG GTATCCCTCA GGG

23

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

AGACCAAAGG AATTCCATCA GGCTCAATTC TGTCATCTTT TTTGTGTCAT TTCTATATGG

60

AAGATTTGAT TGATGAATAC CTATCGTTTA CGAAAAAGAA AGGATCAGTG TTGTTACGAG

120

TAGTCGACGA CTACCTCCTC ATCACC

146

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Gly Ile Pro Ser Gly Ser Ile Leu Ser Ser Phe Leu Cys His Phe  
1 5 10 15  
Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe Thr Lys Lys Lys  
20 25 30  
Gly Ser Val Leu Leu Arg Val Val Asp Asp Tyr Leu Leu Ile Thr  
35 40 45

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GACGATTTC TCTTTATAAC A

21

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Asp Phe Leu Phe Ile Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAAAAAAAAA AAAAAA

16

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTTTTTTTTT TTTTTTTT

17

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Trp	Leu	Tyr	Asn	Ser	Phe	Ile	Ile	Pro	Ile	Leu	Gln	Ser	Phe	Phe	Tyr
1				5				10						15	
Ile	Thr	Glu	Ser	Ser	Asp	Leu	Arg	Asn	Arg	Thr	Val	Tyr	Phe	Arg	Lys
		20					25						30		
Asp	Ile	Trp													
		35													

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Schizosaccharomyces pombe tez1p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Val	Ile	Arg	Leu	Leu	Pro	Lys	Lys	Asn	Thr	Phe	Arg	Leu	Ile	Thr
1				5					10				15		

Asn Leu Arg Lys Arg Phe  
20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..26  
(D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg Ile  
1 5 10 15

Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..32  
(D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile Leu Ser Ser Phe  
1 5 10 15

Leu Cys His Phe Tyr Met Glu Asp Leu Ile Asp Glu Tyr Leu Ser Phe  
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from Schizosaccharomyces pombe tezlp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile Thr Val Asn Lys
1           5           10           15
Lys Asp Ala Lys Lys Phe Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys
          20           25           30
His Asn Phe Ser Thr Ser Leu Glu Lys Thr Val Ile Asn Phe Glu Asn
          35           40           45
Ser

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: /note= "motif 0 peptide from Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Trp Leu Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr
1           5           10           15
Cys Thr Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp
          20           25           30
Thr Trp

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..25
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu Phe Arg Ile  
1                      5                      10                      15  
Ile Ala Ile Pro Cys Arg Gly Ala Asp  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from  
Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile  
1                      5                      10                      15  
Pro Arg Met Glu Cys Met Arg Ile Leu Lys  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..32  
 (D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro  
 1                      5                      10                      15  
 Ile Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe  
                     20                      25                      30

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..49  
 (D) OTHER INFORMATION: /note= "motif 5(C) peptide from  
 Saccharomyces cerevisiae EST2p"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile Ser Thr Asp Gln  
 1                      5                      10                      15  
 Gln Gln Val Ile Asn Ile Lys Lys Leu Ala Met Gly Gly Phe Gln Lys  
                     20                      25                      30  
 Tyr Asn Ala Lys Ala Asn Arg Asp Lys Ile Leu Ala Val Ser Ser Gln  
                     35                      40                      45  
 Ser

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..35  
 (D) OTHER INFORMATION: /note= "motif 0 peptide from  
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Trp Ile Phe Glu Asp Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr  
1 5 10 15  
Val Thr Glu Gln Gln Lys Ser Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys  
20 25 30  
Asn Ile Trp  
35

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..23
- (D) OTHER INFORMATION: /note= "motif 1 and 2 peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gly Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met  
1 5 10 15  
Thr Phe Asn Lys Lys Ile Val  
20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..26
- (D) OTHER INFORMATION: /note= "motif 3(A) peptide from Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser Val  
1 5 10 15



Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..32  
 (D) OTHER INFORMATION: /note= "motif 4(B') peptide from  
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys Val Ser Ser Ile  
1 5 10 15  
 Leu Ser Ser Phe Tyr Tyr Ala Thr Leu Glu Glu Ser Ser Leu Gly Phe  
20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..49  
 (D) OTHER INFORMATION: /note= "motif 5(C) and 6(D) peptide from  
 Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile Thr Thr Gln Glu  
1 5 10 15  
 Asn Asn Ala Val Leu Phe Ile Glu Lys Leu Ile Asn Val Ser Arg Glu  
20 25 30  
 Asn Gly Phe Lys Phe Asn Met Lys Lys Leu Gln Thr Ser Phe Pro Leu  
35 40 45  
 Ser

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif 1 peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Leu Val Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln  
1                      5                      10                      15  
Lys Ser Tyr Ser Lys Thr  
                    20

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "motif 0 peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Lys Ser Leu Gly Phe Ala Pro Gly Lys Leu Arg Leu Ile Pro Lys Lys  
1                      5                      10                      15  
Thr Thr Phe Arg Pro Ile Met Thr Phe Asn Lys Lys Ile Val  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif A peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr Asp Ser  
1 5 10 15

Val Asn Arg Glu Lys Leu Ser Thr Phe Leu Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Asn Gly Lys Phe Tyr Lys Gln Thr Lys Gly Ile Pro Gln Gly Leu Cys  
1 5 10 15

Val Ser Ser Ile Leu Ser Ser Phe Tyr Tyr Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 22

(D) OTHER INFORMATION: /note= "motif C peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Pro Asn Val Asn Leu Leu Met Arg Leu Thr Asp Asp Tyr Leu Leu Ile  
1                   5                   10                   15  
Thr Thr Gln Glu Asn Asn  
                  20

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "motif D peptide from  
Euplotes aediculatus p123"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Asn Val Ser Arg Glu Asn Gly Phe Lys Phe Asn Met Lys Lys Leu  
1                   5                   10                   15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "motif 1 peptide from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Ile Ile Pro Ile Leu Gln Ser Phe Phe Tyr Ile Thr Glu Ser Ser  
1                   5                   10                   15  
Asp Leu Arg Asn Arg Thr  
                  20

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "motif 0 peptide from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Gln Lys Thr Thr Leu Pro Pro Ala Val Ile Arg Leu Leu Pro Lys Lys  
1 5 10 15

Asn Thr Phe Arg Leu Ile Thr Asn Leu Arg Lys Arg Phe Leu  
20 25 30

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..27  
(D) OTHER INFORMATION: /note= "motif A peptide from  
Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Arg Lys Lys Tyr Phe Val Arg Ile Asp Ile Lys Ser Cys Tyr Asp Arg  
1 5 10 15

Ile Lys Gln Asp Leu Met Phe Arg Ile Val Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Gly Asn Ser Gln Tyr Leu Gln Lys Val Gly Ile Pro Gln Gly Ser Ile  
1                      5                      10                      15  
Leu Ser Ser Phe Leu Cys His Phe Tyr Met Glu  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "motif C peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Lys Lys Gly Ser Val Leu Leu Arg Val Val Asp Asp Phe Leu Phe Ile  
1                      5                      10                      15  
Thr Val Asn Lys Lys Asp  
                    20

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "motif D peptide from Schizosaccharomyces pombe tez1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Leu Asn Leu Ser Leu Arg Gly Phe Glu Lys His Asn Phe Ser Thr  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..22  
 (D) OTHER INFORMATION: /note= "motif 1 peptide from  
 Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr Glu Ile Ser  
 1 5 10 15  
 Ser Thr Val Thr Ile Val  
 20

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..32  
 (D) OTHER INFORMATION: /note= "motif 0 peptide from  
 Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Leu Ser Asn Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys  
 1 5 10 15  
 Ser Asn Asn Glu Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 amino acids  
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif A peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro Glu Leu Tyr Phe Met Lys Phe Asp Val Lys Ser Cys Tyr Asp Ser  
1                      5                      10                      15  
  
Ile Pro Arg Met Glu Cys Met Arg Ile Leu Lys  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..27
- (D) OTHER INFORMATION: /note= "motif B peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Glu Asp Lys Cys Tyr Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser  
1                      5                      10                      15  
  
Leu Ser Ala Pro Ile Val Asp Leu Val Tyr Asp  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide



(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "motif C peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe Leu Ile Ile  
1 5 10 15  
Ser Thr Asp Gln Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "motif D peptide from  
Saccharomyces cerevisiae EST2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys Lys Leu Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..22  
(D) OTHER INFORMATION: /note= "motif 1 peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr  
1 5 10 15  
Phe Gln Lys Asn Arg Leu  
20

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: /note= "motif 0 peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Ala Arg Pro Ala Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
1                   5                   10                   15  
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
          20                   25                   30

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide  
(B) LOCATION: 1..27  
(D) OTHER INFORMATION: /note= "motif A peptide from human  
telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr  
1                   5                   10                   15  
Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala  
          20                   25

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..27

(D) OTHER INFORMATION: /note= "motif B peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Arg Ala Thr Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile  
1 5 10 15

Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..22

(D) OTHER INFORMATION: /note= "motif C peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val  
1 5 10 15

Thr Pro His Leu Thr His  
20

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /note= "motif D peptide from human telomerase core protein 1 (TCP1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Phe Phe Tyr Val Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4029 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY:  
(B) LOCATION: 1..4029  
(D) OTHER INFORMATION: /note= "preliminary sequence for  
human TRT cDNA insert of  
plasmid pGRN121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCGATGCC 60  
GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC AGCCACTACC GCGAGGTGCT 120  
GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG 180  
GGACCCGGCG GCTTTCCGCG CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN 240  
ANGGCNGCCC CCCGCCGCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC 300  
CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT TCGGCTTCGC 360  
GCTGCTGGAC GGGGCCCCGCG GGGGCCCCC CGAGGCCTTC ACCACCAGCG TGCGCAGCTA 420  
CCTGCCCAAC ACGGTGACCG ACGCACTGCG GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG 480  
CCGCGTGGGC GACGACGTGC TGGTTCACCT GCTGGCACGC TCGCGNTNT TTGTGCTGGT 540

GGNTCCAGC	TGCGCCTACC	ANGTGTGCGG	GCCGCCGCTG	TACCAGCTCG	GCGCTGCNAC	600
TCAGGCCCCG	CCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC	CAACGGGCCT	660
GGAACCATAG	CGTCAGGGAG	GCCGGGGTCC	CCCTGGGCTG	CCAGCCCCGG	GTGCGAGGAG	720
GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC	GTTGCCCAAG	AGGCCCAGGC	GTGGCGCTGC	780
CCCTGAGCCG	GAGCGGACGC	CCGTTGGGCA	GGGGTCTCTG	GCCCACCCGG	GCAGGACGCC	840
TGGACCGAGT	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAAGCCAC	900
CTCTTTGGAG	GGTGCCTCT	CTGGCACGCG	CCACTCCCAC	CCATCCGTGG	GCCGCCAGCA	960
CCACGCGGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCCT	GGGACACGCC	TTGTCCCCCG	1020
GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	1080
CTTCCTACTC	AATATATCTG	AGGCCCAGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	1140
NTCTTTCTGG	TTCCAGGCCCT	TGGATGCCAG	GATTCCCCGC	AGGTTGCCCC	GCCTGCCCCA	1200
GCGNTACTGG	CAAATGCGGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG	CGCAGTGCCC	1260
CTACGGGGTG	TTCTCAAGA	CGCACTGCCC	GCTGCGAGCT	GCGGTCACCC	CAGCAGCCGG	1320
TGTCTGTGCC	CGGGAGAAGC	CCCAGGGCTC	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	1380
ACCCCCGTCG	CCTGGTGCAG	CTGCTCCGCC	AGCACAGCAG	CCCCTGGCAG	GTGTACGGCT	1440
TCGTGCGGGC	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGCCCT	CTGGGGCTCC	AGGCACAACG	1500
AACGCCGCTT	CCTCAGGAAC	ACCAAGAAGT	TCATCTCCCT	GGGGAAGCAT	GCCAAGCTCT	1560
CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG	CGCTTGCTG	CGCAGGAGCC	1620
CAGGGGTTGG	CTGTGTTCCG	GCCGCAGAGC	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	1680
TCCTGCACTG	GCTGATGAGT	GTGTACGTGC	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	1740
CGGAGACCAC	GTTTCAAAAG	AACAGGCTCT	TTTTCTACCG	GAAGAGTGTC	TGGAGCAAGT	1800
TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG	CTGTGGAAG	1860
CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT	GACGTCCAGA	CTCCGCTTCA	1920
TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG	TGAACATGGA	CTACGTCGTG	GGAGCCAGAA	1980
CGTTCCGCAG	AGAAAAGAGG	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTACGCG	2040
TGCTCAACTA	CGAGCGGGCG	CGGCGCCCCG	GCCTCCTGGG	CGCCTCTGTG	CTGGGCCTGG	2100
ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	GCGGGCCCAG	GACCCGCCGC	2160
CTGAGCTGTA	CTTTGTCAAG	GTGGATGTGA	CGGGCGCGTA	CGACACCATC	CCCCAGGACA	2220
GGCTCACGGA	GGTCATCGCC	AGCATCATCA	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	2280
ATGCCGTGGT	CCAGAAGGCC	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	2340
CTACCTTGAC	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAAACA	2400

GECCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG	GCCAGCAGTG	2460
GCCTCTTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACCACGC	CGTGCGCATC	AGGGGCAAGT	2520
CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	2580
TGTGCTACGG	CGACATGGAG	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	2640
TGCGTTTGGT	GGATGATTTT	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTCC	2700
TCAGGACCCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACCTG	CGGAAGACAG	2760
TGGTGAACCT	CCCTGTAGAA	GACGAGGCC	TGGGTGGCAC	GGCTTTTGTT	CAGATGCCGG	2820
CCCACGGCCT	ATTCCCCTGG	TGCGGCCTGC	TGCTGGATAC	CCGGACCCTG	GAGGTGCAGA	2880
GCGACTACTC	CAGCTATGCC	CGGACCTCCA	TCAGAGCCAG	TCTCACCTTC	AACCGCGGCT	2940
TCAAGGCTGG	GAGGAACATG	CGTCGCAAAC	TCTTTGGGGT	CTTGCGGCTG	AAGTGTCA	3000
GCCTGTTTTCT	GGATTTGCAG	GTGAACAGCC	TCCAGACGGT	GTGCACCAAC	ATCTACAAGA	3060
TCCTCCTGCT	GCAGGCGTAC	AGGTTTCACG	CATGTGTGCT	GCAGCTCCCA	TTTCATCAGC	3120
AAGTTTGGA	GAACCCACA	TTTTTCCTGC	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	3180
ACTCCATCCT	GAAAGCCAAG	AACGCAGGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	3240
CTCTGCCCTC	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAGC	ATCCTGCTC	AAGCTGACTC	3300
GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG	ACGCAGCTGA	3360
GTCGGAAGCT	CCCGGGGACG	ACGCTGACTG	CCCTGGAGGC	CGCAGCCAAC	CCGGCACTGC	3420
CCTCAGACTT	CAAGACCATC	CTGGACTGAT	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	3480
GACACCAGCA	GCCCTGTAC	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCCACAC	3540
CCAGGCCCGC	ACCGTGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGGCCGAG	GCCTGCATGT	3600
CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCCAA	GGGCTGAGTG	3660
TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG	CTCGGCTCCA	CCCCAGGGCC	3720
AGCTTTTCCT	CACCAGGAGC	CCGGCTTCCA	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	3780
TTCGCCATTG	TTCACCCCTC	GCCCTGCCCT	CCTTTGCCTT	CCACCCCCAC	CATCCAGGTG	3840
GAGACCCTGA	GAAGGACCCT	GGGAGCTCTG	GGAATTTGGA	GTGACCAAAG	GTGTGCCCTG	3900
TACACAGGCG	AGGACCCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT	GGGGGAGGT	3960
GCTGTGGGAG	TAAATACTG	AATATATGAG	TTTTTCAGTT	TTGAAAAAAA	AAAAAAAAAA	4020
AAAAAAAAAA						4029

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 261 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ala	Ala	Leu	Arg	Pro	Ala	Ala	His	Val	Gly	Ser	Pro	Gly	Pro	Gly	His	1	5	10	15
Pro	Arg	Asp	Ala	Ala	Arg	Ser	Pro	Leu	Pro	Ser	Arg	Ala	Leu	Pro	Ala	20	25	30	
Ala	Gln	Pro	Leu	Pro	Arg	Gly	Ala	Ala	Gly	His	Val	Arg	Ala	Ala	35	40	45		
Pro	Gly	Ala	Pro	Gly	Leu	Ala	Ala	Gly	Ala	Ala	Arg	Gly	Pro	Gly	Gly	50	55	60	
Phe	Pro	Arg	Xaa	Gly	Gly	Pro	Xaa	Xaa	Gly	Val	Arg	Ala	Leu	Gly	Xaa	65	70	75	80
Xaa	Ala	Ala	Pro	Arg	Arg	Pro	Leu	Leu	Pro	Pro	Gly	Val	Leu	Pro	Glu	85	90	95	
Xaa	Xaa	Gly	Gly	Pro	Ser	Ala	Ala	Xaa	Ala	Val	Arg	Xaa	Arg	Arg	Glu	100	105	110	
Xaa	Arg	Ala	Gly	Leu	Arg	Leu	Arg	Ala	Ala	Gly	Arg	Gly	Pro	Arg	Gly	115	120	125	
Pro	Pro	Arg	Gly	Leu	His	His	Gln	Arg	Ala	Gln	Leu	Pro	Ala	Gln	His	130	135	140	
Gly	Asp	Arg	Arg	Thr	Ala	Gly	Glu	Arg	Gly	Val	Gly	Ala	Ala	Ala	Ala	145	150	155	160
Pro	Arg	Gly	Arg	Arg	Arg	Ala	Gly	Ser	Pro	Ala	Gly	Thr	Leu	Arg	Xaa	165	170	175	
Xaa	Cys	Ala	Gly	Gly	Ser	Gln	Leu	Arg	Leu	Pro	Xaa	Val	Arg	Ala	Ala	180	185	190	
Ala	Val	Pro	Ala	Arg	Arg	Cys	Xaa	Ser	Gly	Pro	Ala	Pro	Ala	Thr	Arg	195	200	205	
Xaa	Trp	Thr	Arg	Xaa	Arg	Leu	Gly	Ser	Asn	Gly	Pro	Gly	Thr	Ile	Ala	210	215	220	
Ser	Gly	Arg	Pro	Gly	Ser	Pro	Trp	Ala	Ala	Ser	Pro	Gly	Cys	Glu	Glu	225	230	235	240
Ala	Arg	Gly	Gln	Cys	Gln	Pro	Lys	Ser	Ala	Val	Ala	Gln	Glu	Ala	Gln	245	250	255	
Ala	Trp	Arg	Cys	Pro	260														

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Ala Gly Ala Asp Ala Arg Trp Ala Gly Val Leu Gly Pro Pro Gly Gln  
 1                      5                      10                      15  
 Asp Ala Trp Thr Glu  
                     20

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Pro Trp Phe Leu Cys Gly Val Thr Cys Gln Thr Arg Arg Arg Ser His  
 1                      5                      10                      15  
 Leu Phe Gly Gly Cys Ala Leu Trp His Ala Pro Leu Pro Pro Ile Arg  
                     20                      25                      30  
 Gly Pro Pro Ala Pro Arg Gly Pro Pro Ile His Ile Ala Ala Thr Thr  
                     35                      40                      45  
 Ser Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe  
                     50                      55                      60  
 Leu Tyr Ser Ser Gly Asp Lys Xaa Thr Ala Xaa Leu Leu Pro Thr Gln  
 65                      70                      75                      80  
 Tyr Ile

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:



Leu Ala Phe Gly Arg Phe Val Glu Thr Xaa Phe Leu Val Pro Gly Leu  
 1 5 10 15  
 Gly Cys Gln Asp Ser Pro Gln Val Ala Pro Pro Ala Pro Ala Xaa Leu  
 20 25 30  
 Ala Asn Ala Ala Pro Val Ser Gly Ala Ala Trp Glu Pro Arg Ala Val  
 35 40 45  
 Pro Leu Arg Gly Val Pro Gln Asp Ala Leu Pro Ala Ala Ser Cys Gly  
 50 55 60  
 His Pro Ser Ser Arg Cys Leu Cys Pro Gly Glu Ala Pro Gly Leu Cys  
 65 70 75 80  
 Gly Gly Pro Arg Gly Gly Gly Thr Gln Thr Pro Val Ala Trp Cys Ser  
 85 90 95  
 Cys Ser Ala Ser Thr Ala Ala Pro Gly Arg Cys Thr Ala Ser Cys Gly  
 100 105 110  
 Pro Ala Cys Ala Gly Trp Cys Pro Gln Ala Ser Gly Ala Pro Gly Thr  
 115 120 125  
 Thr Asn Ala Ala Ser Ser Gly Thr Pro Arg Ser Ser Ser Pro Trp Gly  
 130 135 140  
 Ser Met Pro Ser Ser Arg Cys Arg Ser  
 145 150

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Ala Cys Gly Thr Ala Leu Gly Cys Ala Gly Ala Gln Gly Leu Ala Val  
 1 5 10 15  
 Phe Arg Pro Gln Ser Thr Val Cys Val Arg Arg Ser Trp Pro Ser Ser  
 20 25 30  
 Cys Thr Gly  
 35

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Val Cys Thr Ser Ser Ser Cys Ser Gly Leu Ser Phe Met Ser Arg Arg  
1 5 10 15  
Pro Arg Phe Lys Arg Thr Gly Ser Phe Ser Thr Gly Arg Val Ser Gly  
20 25 30  
Ala Ser Cys Lys Ala Leu Glu Ser Asp Ser Thr  
35 40

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg Gly Cys Ser Cys Gly Ser Cys Arg Lys Gln Arg Ser Gly Ser Ile  
1 5 10 15  
Gly Lys Pro Gly Pro Pro Cys  
20

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Arg Pro Asp Ser Ala Ser Ser Pro Ser Leu Thr Gly Cys Gly Arg Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Thr Trp Thr Thr Ser Trp Glu Pro Glu Arg Ser Ala Glu Lys Arg Gly  
1 5 10 15  
Pro Ser Val Ser Pro Arg Gly  
20

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Arg His Cys Ser Ala Cys Ser Thr Thr Ser Gly Arg Gly Ala Pro Ala  
1 5 10 15  
Ser Trp Ala Pro Leu Cys Trp Ala Trp Thr Ile Ser Thr Gly Pro Gly  
20 25 30  
Ala Pro Ser Cys Cys Val Cys Gly Pro Arg Thr Arg Arg Leu Ser Cys  
35 40 45  
Thr Leu Ser Arg Trp Met  
50

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Arg Ala Arg Thr Thr Pro Ser Pro Arg Thr Gly Ser Arg Arg Ser Ser  
1 5 10 15  
Pro Ala Ser Ser Asn Pro Arg Thr Arg Thr Ala Cys Val Gly Met Pro  
20 25 30  
Trp Ser Arg Arg Pro Pro Met Gly Thr Ser Ala Arg Pro Ser Arg Ala  
35 40 45  
Thr Ser Leu Pro  
50

(2) INFORMATION FOR SEQ ID NO:185:

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Thr Ala Arg

(ii) MOLECULE TYPE: peptide

1				Ser	Ser	Ser	Ser	Arg	Ala	Pro	Pro
				5						10	

(ii) MOLECULE TYPE: peptide

Ser Cys Val Trp Trp Met Ile Ser Cys Trp  
65 70

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

His Leu Thr Ser Pro Thr Arg Lys Pro Ser Ser Gly Pro Trp Ser Glu  
1 5 10 15  
Val Ser Leu Ser Met Ala Ala Trp  
20

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Thr Cys Gly Arg Gln Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Lys Thr Arg Pro Trp Val Ala Arg Leu Leu Phe Arg Cys Arg Pro Thr  
1 5 10 15  
Ala Tyr Ser Pro Gly Ala Ala Cys Cys Trp Ile Pro Gly Pro Trp Arg  
20 25 30  
Cys Arg Ala Thr Thr Pro Ala Met Pro Gly Pro Pro Ser Glu Pro Val  
35 40 45  
Ser Pro Ser Thr Ala Ala Ser Arg Leu Gly Gly Thr Cys Val Ala Asn  
50 55 60

Ser Leu Gly Ser Cys Gly  
65 70

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Ser Val Thr Ala Cys Phe Trp Ile Cys Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Thr Ala Ser Arg Arg Cys Ala Pro Thr Ser Thr Arg Ser Ser Cys Cys  
1 5 10 15  
 Arg Arg Thr Gly Phe Thr His Val Cys Cys Ser Ser His Phe Ile Ser  
20 25 30  
 Lys Phe Gly Arg Thr Pro His Phe Ser Cys Ala Ser Ser Leu Thr Arg  
35 40 45  
 Pro Pro Ser Ala Thr Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Lys Pro Arg Thr Gln Gly Cys Arg Trp Gly Pro Arg Ala Pro Pro Ala  
1 5 10 15

Leu Cys Pro Pro Arg Pro Cys Ser Gly Cys Ala Thr Lys His Ser Cys  
 20 25 30  
 Ser Ser

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Leu Asp Thr Val Ser Pro Thr Cys His Ser Trp Gly His Ser Gly Gln  
 1 5 10 15  
 Pro Arg Arg Ser  
 20

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Val Gly Ser Ser Arg Gly Arg Arg  
 1 5

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Pro Trp Arg Pro Gln Pro Thr Arg His Cys Pro Gln Thr Ser Arg  
 1 5 10 15  
 Pro Ser Trp Thr Asp Gly His Pro Pro Thr Ala Arg Pro Arg Ala Asp  
 20 25 30

Thr Ser Ser Pro Val Thr Pro Gly Ser Thr Ser Gln Gly Gly Arg Gly  
 35 40 45

Gly Pro His Pro Gly Pro His Arg Trp Glu Ser Glu Ala  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Val Ser Val Trp Pro Arg Pro Ala Cys Pro Ala Glu Gly  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Gly Leu Ser Glu Cys Pro Ala Lys Gly  
 1 5

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Val Ser Ser Thr Pro Ala Val Phe Thr Ser Pro Gln Ala Gly Ala Arg  
 1 5 10 15

Leu His Pro Arg Ala Ser Phe Ser Ser Pro Gly Ala Arg Leu Pro Leu  
 20 25 30

Pro Thr



(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Ser Ile Pro Arg Phe Ala Ile Val His Pro Ser Pro Cys Pro Pro Leu  
1 5 10 15  
Pro Ser Thr Pro Thr Ile Gln Val Glu Thr Leu Arg Arg Thr Leu Gly  
20 25 30  
Ala Leu Gly Ile Trp Ser Asp Gln Arg Cys Ala Leu Tyr Thr Gly Glu  
35 40 45  
Asp Pro Ala Pro Gly Trp Gly Ser Leu Trp Val Lys Leu Gly Gly Gly  
50 55 60  
Ala Val Gly Val Lys Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Ile Tyr Glu Phe Phe Ser Phe Glu Lys Lys Lys Lys Lys Lys Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Arg Cys Val Leu Leu Arg Thr Trp Glu Ala Leu Ala Pro Ala Thr  
1 5 10 15

Pro Ala Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu  
20 25 30

Arg Ser His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg  
35 40 45

Leu Gly Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala  
50 55 60

Phe Arg Ala Xaa Val Ala Xaa Cys Xaa Val Cys Val Pro Trp Xaa Xaa  
65 70 75 80

Xaa Xaa Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Xaa  
85 90 95

Xaa Leu Val Ala Arg Val Leu Xaa Xaa Leu Cys Xaa Arg Gly Ala Xaa  
100 105 110

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
115 120 125

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
130 135 140

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
145 150 155 160

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Xaa  
165 170 175

Phe Val Leu Val Xaa Pro Ser Cys Ala Tyr Xaa Val Cys Gly Pro Pro  
180 185 190

Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
195 200 205

Xaa Gly Pro Glu Xaa Val Trp Asp Pro Thr Gly Leu Glu Pro  
210 215 220

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 330 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Arg Gln Gly Gly Arg Gly Pro Pro Gly Leu Pro Ala Pro Gly Ala Arg  
1 5 10 15

Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
20 25 30

Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
35 40 45

Ser Trp Ala His Pro Gly Arg Thr Pro Gly Pro Ser Asp Arg Gly Phe  
 50 55 60  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 65 70 75 80  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 85 90 95  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Gly Thr  
 100 105 110  
 Arg Leu Val Pro Arg Cys Thr Pro Arg Pro Ser Thr Ser Ser Thr Pro  
 115 120 125  
 Gln Ala Thr Xaa Thr Leu Arg Pro Ser Phe Leu Leu Asn Ile Ser Glu  
 130 135 140  
 Ala Gln Pro Asp Trp Arg Ser Gly Gly Ser Trp Arg Xaa Ser Phe Trp  
 145 150 155 160  
 Phe Gln Ala Leu Asp Ala Arg Ile Pro Arg Arg Leu Pro Arg Leu Pro  
 165 170 175  
 Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn  
 180 185 190  
 His Ala Gln Cys Pro Tyr Gly Val Phe Leu Lys Thr His Cys Pro Leu  
 195 200 205  
 Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro  
 210 215 220  
 Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Glu His Arg Pro Pro Ser  
 225 230 235 240  
 Pro Gly Ala Ala Ala Pro Pro Ala Gln Gln Pro Leu Ala Gly Val Arg  
 245 250 255  
 Leu Arg Ala Gly Leu Pro Ala Pro Ala Gly Ala Pro Arg Pro Leu Gly  
 260 265 270  
 Leu Gln Ala Gln Arg Thr Pro Leu Pro Gln Glu His Gln Glu Val His  
 275 280 285  
 Leu Pro Gly Glu Ala Cys Gln Ala Leu Ala Ala Gly Ala Asp Val Glu  
 290 295 300  
 Asp Glu Arg Ala Gly Leu Arg Leu Ala Ala Gln Glu Pro Arg Gly Trp  
 305 310 315 320  
 Leu Cys Ser Gly Arg Arg Ala Pro Ser Ala  
 325 330

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Asp Pro Gly Gln Val Pro Ala Leu Ala Asp Glu Cys Val Arg Arg  
1 5 10 15  
Arg Ala Ala Gln Val Phe Leu Leu Cys His Gly Asp His Val Ser Lys  
20 25 30  
Glu Gln Ala Leu Phe Leu Pro Glu Glu Cys Leu Glu Gln Val Ala Lys  
35 40 45  
His Trp Asn Gln Thr Ala Leu Glu Glu Gly Ala Ala Ala Gly Ala Val  
50 55 60  
Gly Ser Arg Gly Gln Ala Ala Ser Gly Ser Gln Ala Arg Pro Ala Asp  
65 70 75 80  
Val Gln Thr Pro Leu His Pro Gln Ala  
85

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Arg Ala Ala Ala Asp Cys Glu His Gly Leu Arg Arg Gly Ser Gln Asn  
1 5 10 15  
Val Pro Gln Arg Lys Glu Gly Arg Ala Ser His Leu Glu Gly Glu Gly  
20 25 30  
Thr Val Gln Arg Ala Gln Leu Arg Ala Gly Ala Ala Pro Arg Pro Pro  
35 40 45  
Gly Arg Leu Cys Ala Gly Pro Gly Arg Tyr Pro Gln Gly Leu Ala His  
50 55 60  
Leu Arg Ala Ala Cys Ala Gly Pro Gly Pro Ala Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Ala Val Leu Cys Gln Gly Gly Cys Asp Gly Arg Val Arg His His Pro  
1 5 10 15  
Pro Gly Gln Ala His Gly Gly His Arg Gln His His Gln Thr Pro Glu  
20 25 30  
His Val Leu Arg Ala Ser Val Cys Arg Gly Pro Glu Gly Arg Pro Trp  
35 40 45  
Ala Arg Pro Gln Gly Leu Gln Glu Pro Arg Leu Tyr Leu Asp Arg Pro  
50 55 60  
Pro Ala Val His Ala Thr Val Arg Gly Ser Pro Ala Gly Xaa Gln Pro  
65 70 75 80  
Ala Glu Gly Cys Arg Arg His Arg Ala Glu Leu Leu Pro Glu  
85 90

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Gly Gln Gln Trp Pro Leu Arg Arg Leu Pro Thr Leu His Val Pro Pro  
1 5 10 15  
Arg Arg Ala His Gln Gly Gln Val Leu Arg Pro Val Pro Gly Asp Pro  
20 25 30  
Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg  
35 40 45  
His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro  
50 55 60  
Ala Phe Gly Gly  
65

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Phe Leu Val Gly Asp Thr Ser Pro His Pro Arg Glu Asn Leu Pro Gln  
 1 5 10 15  
 Asp Pro Gly Pro Arg Cys Pro  
 20

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Trp Leu Arg Gly Glu Leu Ala Glu Asp Ser Gly Glu Leu Pro Cys  
 1 5 10 15  
 Arg Arg Arg Gly Pro Gly Trp His Gly Phe Cys Ser Asp Ala Gly Pro  
 20 25 30  
 Arg Pro Ile Pro Leu Val Arg Pro Ala Ala Gly Tyr Pro Asp Pro Gly  
 35 40 45  
 Gly Ala Glu Arg Leu Leu Gln Leu Cys Pro Asp Leu His Gln Ser Gln  
 50 55 60  
 Ser His Leu Gln Pro Arg Leu Gln Gly Trp Glu Glu His Ala Ser Gln  
 65 70 75 80  
 Thr Leu Trp Gly Leu Ala Ala Glu Val Ser Gln Pro Val Ser Gly Phe  
 85 90 95  
 Ala Gly Glu Gln Pro Pro Asp Gly Val His Gln His Leu Gln Asp Pro  
 100 105 110  
 Pro Ala Ala Gly Val Gln Val Ser Arg Met Cys Ala Ala Ala Pro Ile  
 115 120 125  
 Ser Ser Ala Ser Leu Glu Glu Pro His Ile Phe Pro Ala Arg His Leu  
 130 135 140

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

His Gly Leu Pro Leu Leu Leu His Pro Glu Ser Gln Glu Arg Arg Asp



Leu Pro His Arg Leu Ala Leu Gly Ser Thr Pro Gly Pro Ala Phe Pro  
20 25 30  
His Gln Glu Pro Gly Phe His Ser Pro His Arg Asn Ser Pro Ser Pro  
35 40 45  
Asp Ser Pro Leu Phe Thr Pro Arg Pro Ala Leu Leu Cys Leu Pro Pro  
50 55 60  
Pro Pro Ser Arg Trp Arg Pro  
65 70

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Glu Gly Pro Trp Glu Leu Trp Glu Phe Gly Val Thr Lys Gly Val Pro  
1 5 10 15  
Cys Thr Gln Ala Arg Thr Leu His Leu Asp Gly Gly Pro Cys Gly Ser  
20 25 30  
Asn Trp Gly Glu Val Leu Trp Glu  
35 40

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Asn Thr Glu Tyr Met Ser Phe Ser Val Leu Lys Lys Lys Lys Lys Lys  
1 5 10 15  
Lys Lys

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Ser Ala Ala Ser Cys Cys Ala Arg Gly Lys Pro Trp Pro Arg Pro Pro  
1 5 10 15  
Pro Arg Cys Arg Ala Leu Pro Ala Ala Glu Pro Cys Ala Pro Cys Cys  
20 25 30  
Ala Ala Thr Thr Ala Arg Cys Cys Arg Trp Pro Arg Ser Cys Gly Ala  
35 40 45  
Trp Gly Pro Arg Ala Gly Gly Trp Cys Ser Ala Gly Thr Arg Arg Leu  
50 55 60  
Ser Ala Arg Trp Trp Pro Xaa Ala Trp Cys Ala Cys Pro Gly Xaa Xaa  
65 70 75 80  
Gly Xaa Pro Pro Pro Pro Pro Ser Ala Arg Cys Pro Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Xaa Xaa Trp Trp Pro Glu Cys Cys Xaa Xaa Cys Ala Xaa Ala Ala Arg  
1 5 10 15  
Xaa Thr Cys Trp Pro Ser Ala Ser Arg Cys Trp Thr Gly Pro Ala Gly  
20 25 30  
Ala Pro Pro Arg Pro Ser Pro Pro Ala Cys Ala Ala Thr Cys Pro Thr  
35 40 45  
Arg

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1003 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Pro Thr His Cys Gly Gly Ala Gly Arg Gly Gly Cys Cys Cys Ala Ala  
1 5 10 15

Trp Ala Thr Thr Cys Trp Phe Thr Cys Trp His Ala Ala Arg Xaa Leu  
20 25 30

Cys Trp Trp Xaa Pro Ala Ala Pro Thr Xaa Cys Ala Gly Arg Arg Cys  
35 40 45

Thr Ser Ser Ala Leu Xaa Leu Arg Pro Gly Pro Arg His Thr Leu Xaa  
50 55 60

Asp Pro Xaa Ala Ser Gly Ile Gln Arg Ala Trp Asn His Ser Val Arg  
65 70 75 80

Glu Ala Gly Val Pro Leu Gly Cys Gln Pro Arg Val Arg Gly Gly Ala  
85 90 95

Gly Ala Val Pro Ala Glu Val Cys Arg Cys Pro Arg Gly Pro Gly Val  
100 105 110

Ala Leu Pro Leu Ser Arg Ser Gly Arg Pro Leu Gly Arg Gly Pro Gly  
115 120 125

Pro Thr Arg Ala Gly Arg Leu Asp Arg Val Thr Val Val Ser Val Trp  
130 135 140

Cys His Leu Pro Asp Pro Pro Lys Lys Pro Pro Leu Trp Arg Val Arg  
145 150 155 160

Ser Leu Ala Arg Ala Thr Pro Thr His Pro Trp Ala Ala Ser Thr Thr  
165 170 175

Arg Ala Pro His Pro His Arg Gly His His Val Leu Gly His Ala Leu  
180 185 190

Ser Pro Gly Val Arg Arg Asp Gln Ala Leu Pro Leu Leu Leu Arg Arg  
195 200 205

Gln Xaa His Cys Xaa Pro Pro Ser Tyr Ser Ile Tyr Leu Arg Pro Ser  
210 215 220

Leu Thr Gly Val Arg Glu Val Arg Gly Asp Xaa Leu Ser Gly Ser Arg  
225 230 235 240

Pro Trp Met Pro Gly Phe Pro Ala Gly Cys Pro Ala Cys Pro Ser Xaa  
245 250 255

Thr Gly Lys Cys Gly Pro Cys Phe Trp Ser Cys Leu Gly Thr Thr Arg  
260 265 270

Ser Ala Pro Thr Gly Cys Ser Ser Arg Arg Thr Ala Arg Cys Glu Leu  
275 280 285

Arg Ser Pro Gln Gln Pro Val Ser Val Pro Gly Arg Ser Pro Arg Ala  
290 295 300

Leu Trp Arg Pro Pro Arg Arg Arg Asn Thr Asp Pro Arg Arg Leu Val  
305 310 315 320

Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val  
325 330 335

Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg  
340 345 350

His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu  
355 360 365

Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser  
370 375 380

Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val  
385 390 395 400

Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu  
405 410 415

His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe  
420 425 430

Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg  
435 440 445

Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu  
450 455 460

Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His  
465 470 475 480

Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro  
485 490 495

Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly  
500 505 510

Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg  
515 520 525

Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro  
530 535 540

Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala  
545 550 555 560

Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu  
565 570 575

Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro  
580 585 590

Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn  
595 600 605

Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly  
610 615 620

His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu  
625 630 635 640

Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Xaa Asn Ser Pro  
645 650 655

Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala  
660 665 670

Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala  
 675 680 685  
 Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln  
 690 695 700  
 Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met  
 705 710 715 720  
 Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg  
 725 730 735  
 Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys  
 740 745 750  
 Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val  
 755 760 765  
 Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala  
 770 775 780  
 Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro  
 785 790 795 800  
 Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp  
 805 810 815  
 Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn  
 820 825 830  
 Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val  
 835 840 845  
 Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser  
 850 855 860  
 Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala  
 865 870 875 880  
 Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val  
 885 890 895  
 Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser  
 900 905 910  
 Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly  
 915 920 925  
 Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu  
 930 935 940  
 Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr  
 945 950 955 960  
 Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser Arg  
 965 970 975  
 Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn Pro  
 980 985 990  
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 995 1000

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Trp Pro Pro Ala His Ser Gln Ala Glu Ser Arg His Gln Gln Pro Cys  
1 5 10 15  
His Ala Gly Leu Tyr Val Pro Gly Arg Glu Gly Arg Pro Thr Pro Arg  
20 25 30  
Pro Ala Pro Leu Gly Val  
35

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Gly Leu Ser Glu Cys Leu Ala Glu Ala Cys Met Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Leu Ser Val Arg Leu Arg Pro Glu Arg Val Ser Ser Gln Gly Leu  
1 5 10 15  
Ser Val Gln His Thr Cys Arg Leu His Phe Pro Thr Gly Trp Arg Ser  
20 25 30  
Ala Pro Pro Gln Gly Gln Leu Phe Leu Thr Arg Ser Pro Ala Ser Thr  
35 40 45

Pro His Ile Gly Ile Val His Pro Gln Ile Arg His Cys Ser Pro Leu  
 50 55 60

Ala Leu Pro Ser Phe Ala Phe His Pro His His Pro Gly Gly Asp Pro  
 65 70 75 80

Glu Lys Asp Pro Gly Ser Ser Gly Asn Leu Glu  
 85 90

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Pro Lys Val Cys Pro Val His Arg Arg Gly Pro Cys Thr Trp Met Gly  
 1 5 10 15

Val Pro Val Gly Gln Ile Gly Gly Arg Cys Cys Gly Ser Lys Ile Leu  
 20 25 30

Asn Ile

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Val Phe Gln Phe  
 1

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Lys Lys Lys Lys Lys Lys Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..3454
- (D) OTHER INFORMATION: /product= "hTERT"  
/note= "human telomerase reverse  
transcriptase (hTERT) catalytic protein  
component"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC CCGCG ATG	58
Met	
1	
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC CAC	106
Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser His	
5 10 15	
TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG GGG CCC	154
Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly Pro	
20 25 30	
CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT TTC CGC GCG	202
Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg Ala	
35 40 45	
CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC GCA CGG CCG CCC	250
Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro Pro	
50 55 60 65	
CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC CTG AAG GAG CTG GTG	298
Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu Val	
70 75 80	
GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC GGC GCG AAG AAC GTG CTG	346
Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu	
85 90 95	
GCC TTC GGC TTC GCG CTG CTG GAC GGG GCC CGC GGG GGC CCC CCC GAG	394
Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu	
100 105 110	
GCC TTC ACC ACC AGC GTG CGC AGC TAC CTG CCC AAC ACG GTG ACC GAC	442
Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp	
115 120 125	

GCA	CTG	CGG	GGG	AGC	GGG	GCG	TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	490
Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	
130					135					140					145	
GAC	GAC	GTG	CTG	GTT	CAC	CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	538
Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	
				150					155					160		
GTG	GCT	CCC	AGC	TGC	GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	586
Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	
			165				170						175			
CTC	GGC	GCT	GCC	ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	634
Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	
		180					185					190				
CGA	AGG	CGT	CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	682
Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	
		195				200					205					
GCC	GGG	GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	730
Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	
210					215					220					225	
GGC	AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC	778
Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	
				230					235					240		
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG	GCC	826
Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	
			245					250						255		
CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT	GTG	GTG	874
His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	
		260					265					270				
TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG	GGT	GCG	CTC	922
Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	
		275				280					285					
TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC	CAG	CAC	CAC	GCG	970
Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	
				295					300						305	
GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC	TGG	GAC	ACG	CCT	TGT	1018
Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	
				310					315					320		
CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC	CTC	TAC	TCC	TCA	GGC	GAC	1066
Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	
			325					330					335			
AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA	CTC	AGC	TCT	CTG	AGG	CCC	AGC	1114
Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	
		340					345					350				
CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG	GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	1162
Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	
		355				360					365					
CCC	TGG	ATG	CCA	GGG	ACT	CCC	CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	1210
Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	



370					375					380					385	
TAC	TGG	CAA	ATG	CGG	CCC	CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	1258
Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	
				390					395					400		
CAG	TGC	CCC	TAC	GGG	GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	1306
Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	
			405					410					415			
GCG	GTC	ACC	CCA	GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GGC	1354
Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	
		420					425					430				
TCT	GTG	GCG	GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	1402
Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	Val	
	435					440					445					
CAG	CTG	CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	GGC	TTC	GTG	1450
Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	Val	
450				455				460							465	
CGG	GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	1498
Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	Arg	
				470				475						480		
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	CTG	1546
His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser	Leu	
			485					490					495			
GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	ATG	AGC	1594
Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met	Ser	
		500				505						510				
GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	GGC	TGT	GTT	1642
Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	
	515					520					525					
CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	GCC	AAG	TTC	CTG	1690
Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	
530					535			540							545	
CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	AGG	TCT	TTC	TTT	1738
His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	
				550					555					560		
TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	CTC	TTT	TTC	TAC	CGG	1786
Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	
			565					570					575			
AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	GGA	ATC	AGA	CAG	CAC	TTG	1834
Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	
		580				585						590				
AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	1882
Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	
	595					600					605					
CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	1930
Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	
610					615					620					625	

AAG CCT GAC GGG CTG CGG CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly 630 635 640	1978
GCC AGA ACG TTC CGC AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg 645 650 655	2026
GTG AAG GCA CTG TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro 660 665 670	2074
GGC CTC CTG GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala 675 680 685	2122
TGG CGC ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu 690 695 700 705	2170
CTG TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro 710 715 720	2218
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn 725 730 735	2266
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC CAT GGG Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly 740 745 750	2314
CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG ACA GAC CTC His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu 755 760 765	2362
CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG GAG ACC AGC CCG Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro 770 775 780 785	2410
CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC TCC CTG AAT GAG GCC Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala 790 795 800	2458
AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC TTC ATG TGC CAC CAC GCC Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala 805 810 815	2506
GTG CGC ATC AGG GGC AAG TCC TAC GTC CAG TGC CAG GGG ATC CCG CAG Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln 820 825 830	2554
GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC CTG TGC TAC GGC GAC ATG Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met 835 840 845	2602
GAG AAC AAG CTG TTT GCG GGG ATT CGG CGG GAC GGG CTG CTC CTG CGT Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg 850 855 860 865	2650
TTG GTG GAT GAT TTC TTG TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys	2698

870								875				880				
ACC Thr	TTC Phe	CTC Leu	AGG Arg 885	ACC Thr	CTG Leu	GTC Val	CGA Arg	GGT Gly 890	GTC Val	CCT Pro	GAG Glu	TAT Tyr	GGC Gly 895	TGC Cys	GTG Val	2746
GTG Val	AAC Asn	TTG Leu 900	CGG Arg	AAG Lys	ACA Thr	GTG Val 905	GTG Val	AAC Asn	TTC Phe	CCT Pro	GTA Val	GAA Glu 910	GAC Asp	GAG Glu	GCC Ala	2794
CTG Leu 915	GGT Gly	GGC Gly	ACG Thr	GCT Ala	TTT Phe	GTT Val 920	CAG Gln	ATG Met	CCG Pro	GCC Ala	CAC His 925	GGC Gly	CTA Leu	TTC Phe	CCC Pro	2842
TGG Trp 930	TGC Cys	GGC Gly	CTG Leu	CTG Leu	CTG Leu 935	GAT Asp	ACC Thr	CGG Arg	ACC Thr 940	CTG Leu	GAG Glu	GTG Val	CAG Gln	AGC Ser	GAC Asp 945	2890
TAC Tyr	TCC Ser	AGC Ser	TAT Tyr 950	GCC Ala	CGG Arg	ACC Thr	TCC Ser	ATC Ile 955	AGA Arg	GCC Ala	AGT Ser	CTC Leu	ACC Thr 960	TTC Phe	AAC Asn	2938
CGC Arg	GGC Gly	TTC Phe 965	AAG Lys	GCT Ala	GGG Gly	AGG Arg	AAC Asn	ATG Met 970	CGT Arg	CGC Arg	AAA Lys	CTC Leu 975	TTT Phe	GGG Gly	GTC Val	2986
TTG Leu	CGG Arg 980	CTG Leu	AAG Lys	TGT Cys	CAC His	AGC Ser 985	CTG Leu	TTT Phe	CTG Leu	GAT Asp	TTG Leu 990	CAG Gln	GTG Val	AAC Asn	AGC Ser	3034
CTC Leu 995	CAG Gln	ACG Thr	GTG Val	TGC Cys	ACC Thr 1000	AAC Asn	ATC Ile	TAC Tyr	AAG Lys	ATC Ile 1005	CTC Leu	CTG Leu	CTG Leu	CAG Gln	GCG Ala	3082
TAC Tyr 1010	AGG Arg	TTT Phe	CAC His	GCA Ala 1015	TGT Cys	GTG Val	CTG Leu	CAG Gln	CTC Leu	CCA Pro 1020	TTT Phe	CAT His	CAG Gln	CAA Gln	GTT Val 1025	3130
TGG Trp	AAG Lys	AAC Asn	CCC Pro 1030	ACA Thr	TTT Phe	TTC Phe	CTG Leu	CGC Arg	GTC Val 1035	ATC Ile	TCT Ser	GAC Asp	ACG Thr	GCC Ala 1040	TCC Ser	3178
CTC Leu	TGC Cys	TAC Tyr 1045	TCC Ser	ATC Ile	CTG Leu	AAA Lys	GCC Ala	AAG Lys 1050	AAC Asn	GCA Ala	GGG Gly	ATG Met 1055	TCG Ser	CTG Leu	GGG Gly	3226
GCC Ala	AAG Lys 1060	GGC Gly	GCC Ala	GCC Ala	GGC Gly	CCT Pro	CTG Leu 1065	CCC Pro	TCC Ser	GAG Glu	GCC Ala 1070	GTG Val	CAG Gln	TGG Trp	CTG Leu	3274
TGC Cys 1075	CAC His	CAA Gln	GCA Ala	TTC Phe	CTG Leu 1080	CTC Leu	AAG Lys	CTG Leu	ACT Thr	CGA Arg	CAC His 1085	CGT Arg	GTC Val	ACC Thr	TAC Tyr	3322
GTG Val 1090	CCA Pro	CTC Leu	CTG Leu	GGG Gly	TCA Ser 1095	CTC Leu	AGG Arg	ACA Thr	GCC Ala 1100	CAG Gln	ACG Thr	CAG Gln	CTG Leu	AGT Ser	CGG Arg 1105	3370
AAG Lys	CTC Leu	CCG Pro	GGG Gly 1110	ACG Thr	ACG Thr	CTG Leu	ACT Thr	GCC Ala 1115	CTG Leu	GAG Glu	GCC Ala	GCA Ala	GCC Ala	AAC Asn 1120	CCG Pro	3418

GCA CTG CCC TCA GAC TTC AAG ACC ATC CTG GAC TGATGGCCAC CCGCCCACAG 3471  
 Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1125 1130  
 CCAGGCCGAG AGCAGACACC AGCAGCCCTG TCACGCCGGG CTCTACGTCC CAGGGAGGGA 3531  
 GGGGCGGCCC ACACCCAGGC CCGCACCGCT GGGAGTCTGA GGCCTGAGTG AGTGTTTGGC 3591  
 CGAGGCCTGC ATGTCCGGCT GAAGGCTGAG TGTCCGGCTG AGGCCTGAGC GAGTGTCCAG 3651  
 CCAAGGGCTG AGTGTCCAGC ACACCTGCCG TCTTCACTTC CCCACAGGCT GGCGCTCGGC 3711  
 TCCACCCCAG GGCCAGCTTT TCCTCACCAG GAGCCCGGCT TCCACTCCCC ACATAGGAAT 3771  
 AGTCCATCCC CAGATTGCGC ATTGTTTACC CCTCGCCCTG CCCTCCTTTG CCTTCCACCC 3831  
 CCACCATCCA GGTGGAGACC CTGAGAAGGA CCCTGGGAGC TCTGGGAATT TGGAGTGACC 3891  
 AAAGGTGTGC CCTGTACACA GGCGAGGACC CTGCACCTGG ATGGGGGTCC CTGTGGGTCA 3951  
 AATTGGGGGG AGGTGCTGTG GGAGTAAAAT ACTGAATATA TGAGTTTTTC AGTTTTGAAA 4011  
 AAAA 4015

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140

Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170		175
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185		190
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220	
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	225	230	235	240
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	245	250		255
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	260	265		270
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	275	280		285
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	290	295	300	
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	305	310	315	320
Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	325	330		335
Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	340	345		350
Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	355	360	365	
Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	370	375	380	
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	385	390	395	400
Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	405	410		415
Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	420	425		430
Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	Arg	Leu	435	440	445	
Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe	450	455	460	
Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser	465	470	475	480

Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
485 490 495

Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
500 505 510

Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
530 535 540

Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
545 550 555 560

Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
565 570 575

Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
580 585 590

Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
595 600 605

His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
645 650 655

Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
660 665 670

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
675 680 685

Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
690 695 700

Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
725 730 735

Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
740 745 750

Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
755 760 765

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
915 920 925

Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
930 935 940

Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe  
945 950 955 960

Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
980 985 990

Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln  
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala  
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu  
1045 1050 1055

Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp  
1060 1065 1070

Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr  
1075 1080 1085

Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser  
1090 1095 1100

Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn  
1105 1110 1115 1120

Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
1125 1130